

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 14:20:21 ; Search time 29.31 Seconds
(without alignments)
1759.518 Million cell updates/sec

Title: US-08-883-036A-2
Perfect score: 440
Sequence: 1 MEGRGNAPASGARRKRRHP.....HLSSGKFMVEGNADSAMS 440

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

SPREMBL_15: *
1: sp._archaea: *
2: sp._bacteria: *
3: sp._fungi: *
4: sp._human: *
5: sp._invertebrate: *
6: sp._mammal: *
7: sp._mhc: *
8: sp._organelle: *
9: sp._phage: *
10: sp._plant: *
11: sp._rodent: *
12: sp._unclassified: *
13: sp._vertebrate: *
14: sp._virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	440	100.0	440	4	014763
2	373	84.8	440	4	015531
3	229	52.0	411	4	015517
4	229	52.0	411	4	015508
5	227	51.6	411	4	014720
6	16	3.6	468	4	000220
7	12	2.7	386	4	09Y604
8	12	2.7	386	4	09UBN6
9	11	2.5	920	2	087342
10	9	2.0	362	14	067645
11	8	1.8	29	10	008065
12	8	1.8	108	10	09LW00
13	8	1.8	121	10	024583
14	8	1.8	223	2	09KXN8
15	8	1.8	257	11	09J7E5
16	8	1.8	259	4	014755
17	8	1.8	288	2	09R1W2
18	8	1.8	299	4	014798
19	8	1.8	341	7	097982

20	8	1.8	364	10	09LHX9	091hx9 oryza sativ
21	8	1.8	541	2	09L2C4	0912c4 streptomyce
22	8	1.8	558	5	09M462	09M462 drosophila
23	8	1.8	592	10	09SPF1	09SPF1 arabidopsis
24	8	1.8	592	10	092SS6	092SS6 arabidopsis
25	8	1.8	708	13	P87363	P87363 gallus gall
26	8	1.8	743	2	09L092	09L092 streptomyce
27	8	1.8	769	5	024971	024971 giardia lam
28	8	1.8	3013	14	092530	092530 hepatitis c
29	7	1.6	39	14	079818	079818 human t-cel
30	7	1.6	39	14	085093	085093 simian t-ce
31	7	1.6	47	2	09KGS9	09KGS9 azotobacter
32	7	1.6	73	2	045259	045259 bradyrhizob
33	7	1.6	75	2	032424	032424 actinobacill
34	7	1.6	75	2	066149	066149 actinobacill
35	7	1.6	75	2	09MX51	09MX51 actinobacill
36	7	1.6	75	2	09S5J4	09S5J4 actinobacill
37	7	1.6	76	2	09MM48	09MM48 actinobacill
38	7	1.6	89	2	09JQT2	09JQT2 neisseria m
39	7	1.6	96	10	09LTK4	09LTK4 arabidopsis
40	7	1.6	97	14	065977	065977 cassava com
41	7	1.6	103	1	026203	026203 methanobact
42	7	1.6	111	11	035152	035152 rattus norv
43	7	1.6	111	11	035153	035153 mus musculu
44	7	1.6	123	2	09PE78	09PE78 xylella fas
45	7	1.6	130	2	053859	053859 mycobacteri
46	7	1.6	131	14	088389	088389 simian t-ce
47	7	1.6	132	2	09X215	09X215 thermotoga
48	7	1.6	143	2	066299	066299 unidentified
49	7	1.6	146	1	059825	059825 sulfolobus
50	7	1.6	149	14	082405	082405 human t-cel
51	7	1.6	149	14	082408	082408 human t-cel
52	7	1.6	151	2	09X854	09X854 streptomyce
53	7	1.6	151	5	09M436	09M436 drosophila
54	7	1.6	152	2	09REK6	09REK6 micrococcus
55	7	1.6	165	5	016258	016258 caenorhabdit
56	7	1.6	170	14	008838	008838 human t-cel
57	7	1.6	170	14	070642	070642 simian t-ce
58	7	1.6	170	14	073454	073454 human t-cel
59	7	1.6	172	5	025313	025313 locusta mig
60	7	1.6	175	10	09LM08	09LM08 arabidopsis
61	7	1.6	181	2	P96237	P96237 mycobacteri
62	7	1.6	187	14	011329	011329 molluscum c
63	7	1.6	193	10	09LZH5	09LZH5 arabidopsis
64	7	1.6	199	11	054789	054789 mus musculu
65	7	1.6	204	5	062190	062190 caenorhabdit
66	7	1.6	204	8	035030	035030 modiolus mo
67	7	1.6	206	2	09K2V1	09K2V1 streptomyce
68	7	1.6	212	10	09ZRU6	09ZRU6 catharanthu
69	7	1.6	213	2	056417	056417 thermus aqu
70	7	1.6	215	2	050970	050970 neisseria g
71	7	1.6	215	2	005128	005128 neisseria g
72	7	1.6	233	10	038718	038718 antirrhinum
73	7	1.6	238	2	09RUD4	09RUD4 delinococcus
74	7	1.6	243	2	09PM74	09PM74 campylobact
75	7	1.6	246	1	027171	027171 methanobact
76	7	1.6	249	2	09S3W7	09S3W7 mastigoclad
77	7	1.6	249	1	027533	027533 methanobact
78	7	1.6	251	1	09YAT4	09YAT4 aetopyrum p
79	7	1.6	258	2	09L1H7	09L1H7 streptomyce
80	7	1.6	261	2	09KAL7	09KAL7 bacillus ha
81	7	1.6	275	2	09PB77	09PB77 xylella fas
82	7	1.6	275	13	091B71	091B71 pagrus majo
83	7	1.6	276	5	09M944	09M944 trypanosoma
84	7	1.6	277	2	024603	024603 arabidopsis
85	7	1.6	278	10	09S154	09S154 comamonas t
86	7	1.6	286	13	057342	057342 coturnix co
87	7	1.6	286	13	042290	042290 gallus gall
88	7	1.6	293	10	041542	041542 triticum ae
89	7	1.6	301	10	09M827	09M827 arabidopsis
90	7	1.6	310	2	066675	066675 aquifex aeo
91	7	1.6	310	5	026044	026044 plasmodium
92	7	1.6	319	2	091L72	091L72 streptomyce

93	7	1.6	321	5	077113	077113	biston betu	166	7	1.6	628	5	09XVS7	09XVS7	caenorhabdi
94	7	1.6	326	2	09KES3	09KES3	baecillus ha	167	7	1.6	645	10	P93825	P93825	arabidopsis
95	7	1.6	327	11	054887	054887	mus musculu	168	7	1.6	647	2	084627	084627	chlamydia t
96	7	1.6	329	2	09ZKY9	09ZKY9	helicobacte	169	7	1.6	649	14	041043	041043	paramecium
97	7	1.6	330	2	025530	025530	helicobacte	170	7	1.6	650	2	09L238	09L238	streptomyce
98	7	1.6	337	2	09X517	09X517	neisseria m	171	7	1.6	669	2	068794	068794	yersinia pe
99	7	1.6	337	2	09RDB8	09RDB8	streptomyce	172	7	1.6	670	2	09RXQ7	09RXQ7	deinococcus
100	7	1.6	337	2	09JY12	09JY12	neisseria m	173	7	1.6	674	2	050431	050431	mycobacteri
101	7	1.6	337	2	09JY13	09JY13	neisseria m	174	7	1.6	695	2	085672	085672	thermanner
102	7	1.6	346	2	09KN66	09KN66	vibrio chol	175	7	1.6	702	5	09RKH4	09RKH4	leishmania
103	7	1.6	346	14	011433	011433	avian adeno	176	7	1.6	704	5	09VIE0	09VIE0	dirosophila
104	7	1.6	348	7	031365	031365	brachydanio	177	7	1.6	709	2	09RKY7	09RKY7	deinococcus
105	7	1.6	353	13	042253	042253	gallus gall	178	7	1.6	714	2	051753	051753	pseudomonas
106	7	1.6	354	10	040506	040506	nicotiana t	179	7	1.6	725	2	09KIMS	09KIMS	vibrio chol
107	7	1.6	356	5	09U901	09U901	dirosophila	180	7	1.6	770	10	09S211	09S211	arabidopsis
108	7	1.6	357	10	09SM98	09SM98	oryza sativ	181	7	1.6	798	3	042698	042698	aspergillus
109	7	1.6	361	4	09UK24	09UK24	homo sapien	182	7	1.6	798	3	059862	059862	aspergillus
110	7	1.6	362	10	09LFG2	09LFG2	arabidopsis	183	7	1.6	801	5	023635	023635	caenorhabdi
111	7	1.6	365	5	09NDY1	09NDY1	leishmania	184	7	1.6	808	9	064330	064330	bacterioph
112	7	1.6	365	13	09W7C0	09W7C0	brachydanio	185	7	1.6	862	5	027446	027446	artemia sal
113	7	1.6	369	13	093345	093345	gallus gall	186	7	1.6	874	5	09VSE3	09VSE3	dirosophila
114	7	1.6	379	2	068640	068640	corynebacte	187	7	1.6	875	2	086394	086394	neisseria m
115	7	1.6	382	5	024812	024812	entamoeba h	188	7	1.6	875	2	09K147	09K147	neisseria m
116	7	1.6	386	9	09XJ99	09XJ99	streptococ	189	7	1.6	880	2	09JST3	09JST3	neisseria m
117	7	1.6	392	5	09NGA0	09NGA0	leishmania	190	7	1.6	907	2	09L248	09L248	streptomyce
118	7	1.6	393	2	088064	088064	streptomyce	191	7	1.6	924	2	09ZIG3	09ZIG3	rhodothermu
119	7	1.6	395	11	09QXZ7	09QXZ7	mus musculu	192	7	1.6	951	5	09X582	09X582	rhodothermu
120	7	1.6	397	2	09ZGA9	09ZGA9	streptomyce	193	7	1.6	951	5	09M388	09M388	dirosophila
121	7	1.6	397	2	09RU94	09RU94	deinococcus	194	7	1.6	969	5	09ND19	09ND19	plasmidium
122	7	1.6	408	2	09RN55	09RN55	streptomyce	195	7	1.6	981	14	087645	087645	sindbis vir
123	7	1.6	409	5	09NSW7	09NSW7	caenorhabdi	196	7	1.6	1108	1	058310	058310	pyrococcus
124	7	1.6	412	2	P70868	P70868	bartonella	197	7	1.6	1110	5	09TYP9	09TYP9	caenorhabdi
125	7	1.6	413	10	049504	049504	arabidopsis	198	7	1.6	1123	5	095027	095027	dirosophila
126	7	1.6	415	2	068994	068994	mycobacteri	199	7	1.6	1158	5	076833	076833	caenorhabdi
127	7	1.6	415	2	09X9Y0	09X9Y0	streptomyce	200	7	1.6	1176	5	004155	004155	dirosophila
128	7	1.6	420	5	09ZK16	09ZK16	helicobacte	201	7	1.6	1245	14	088430	088430	sindbis-lik
129	7	1.6	428	2	09V3V6	09V3V6	dirosophila	202	7	1.6	1245	14	088432	088432	sindbis-lik
130	7	1.6	431	2	006557	006557	mycobacteri	203	7	1.6	1246	14	09YJX5	09YJX5	sindbis-lik
131	7	1.6	431	5	09XZC3	09XZC3	dirosophila	204	7	1.6	1346	2	09ZGT2	09ZGT2	streptomyce
132	7	1.6	436	5	027651	027651	e pyrophosp	205	7	1.6	1525	5	024051	024051	dirosophila
133	7	1.6	438	2	09KYG4	09KYG4	streptomyce	206	7	1.6	1525	5	024305	024305	dirosophila
134	7	1.6	451	2	09KZN3	09KZN3	deinococcus	207	7	1.6	1539	10	09LZJ5	09LZJ5	dirosophila
135	7	1.6	451	11	035254	035254	rattus norv	208	7	1.6	1760	5	09VLF2	09VLF2	dirosophila
136	7	1.6	454	10	09M7Q3	09M7Q3	arabidopsis	209	7	1.6	2006	5	09WFE2	09WFE2	dirosophila
137	7	1.6	463	8	021697	021697	colobus que	210	7	1.6	2204	14	090341	090341	newcastle d
138	7	1.6	463	1	09YFT7	09YFT7	aeropyrum p	211	7	1.6	2204	14	090MH6	090MH6	newcastle d
139	7	1.6	463	10	09M1W3	09M1W3	arabidopsis	212	7	1.6	2354	14	096898	096898	hepatitis g
140	7	1.6	465	14	090P16	090P16	gallid heip	213	7	1.6	3054	14	088507	088507	tobacco etc
141	7	1.6	476	5	09XTT6	09XTT6	caenorhabdi	214	7	1.6	3247	14	065553	065553	bovine heip
142	7	1.6	478	10	09S7R8	09S7R8	arabidopsis	215	7	1.4	27	14	090HU6	090HU6	hepatitis c
143	7	1.6	482	1	054610	054610	halobacteri	216	6	1.4	27	14	090HU4	090HU4	hepatitis c
144	7	1.6	485	2	083862	083862	treponema p	217	6	1.4	27	14	090HU2	090HU2	hepatitis c
145	7	1.6	488	2	056708	056708	vibrio para	218	6	1.4	27	14	090HU2	090HU2	hepatitis c
146	7	1.6	488	5	09U3B8	09U3B8	caenorhabdi	219	6	1.4	30	8	08T156	08T156	corymba ex
147	7	1.6	496	10	09S8S3	09S8S3	arabidopsis	220	6	1.4	33	8	09T2L9	09T2L9	nicotiana t
148	7	1.6	505	2	09KYU8	09KYU8	streptomyce	221	6	1.4	43	8	09K1W8	09K1W8	chlamydia p
149	7	1.6	507	5	017862	017862	caenorhabdi	222	6	1.4	45	8	09TM36	09TM36	cyamidium c
150	7	1.6	520	1	028507	028507	archaeoglob	223	6	1.4	52	6	062790	062790	canis famli
151	7	1.6	521	2	09XOG7	09XOG7	vibrio chol	224	6	1.4	53	2	09I9N0	09I9N0	lactococcus
152	7	1.6	522	2	09ZJ80	09ZJ80	helicobacte	225	6	1.4	53	8	09T9G1	09T9G1	lactococcus
153	7	1.6	523	11	09JUP8	09JUP8	rattus norv	226	6	1.4	54	2	059318	059318	eupla strigio
154	7	1.6	524	4	075587	075587	homo sapien	227	6	1.4	54	13	09IAO0	09IAO0	geospiza sc
155	7	1.6	524	6	09N1R4	09N1R4	canis famli	228	6	1.4	54	13	09IAP8	09IAP8	geospiza sc
156	7	1.6	546	2	09X5T7	09X5T7	streptomyce	229	6	1.4	54	13	09IAP7	09IAP7	geospiza sc
157	7	1.6	570	10	09M7S3	09M7S3	liolium pere	230	6	1.4	54	13	09IAP2	09IAP2	geospiza sc
158	7	1.6	574	10	09LUB7	09LUB7	arabidopsis	231	6	1.4	54	13	09IAP4	09IAP4	geospiza sc
159	7	1.6	575	2	09RRW8	09RRW8	deinococcus	232	6	1.4	59	11	061935	061935	musculu
160	7	1.6	582	2	046042	046042	dirosophila	233	6	1.4	59	14	090676	090676	human herpe
161	7	1.6	588	5	09W4Q7	09W4Q7	dirosophila	234	6	1.4	59	14	090684	090684	human herpe
162	7	1.6	582	2	09Z7Z0	09Z7Z0	chlamydia p	235	6	1.4	59	14	090685	090685	human herpe
163	7	1.6	593	14	098224	098224	molluscum c	236	6	1.4	59	14	090690	090690	human herpe
164	7	1.6	613	5	09VGR8	09VGR8	dirosophila	237	6	1.4	60	6	09XS91	09XS91	equus cabal
165	7	1.6	624	10	048662	048662	cucurbita m	238	6	1.4	60	6	09XS91	09XS91	equus cabal

239	6	1.4	62	8	047585	047585 polioptilla	312	6	1.4	105	2	09S1M8	09S1M8 streptomyce
240	6	1.4	62	8	047586	047586 polioptilla	313	6	1.4	106	11	06Z895	06Z895 ratiu norv
241	6	1.4	62	8	047587	047587 polioptilla	314	6	1.4	105	1	027467	027467 methanobact
242	6	1.4	62	8	047588	047588 polioptilla	315	6	1.4	106	5	09N1O6	09N1O6 trypanosoma
243	6	1.4	62	8	048290	048290 polioptilla	316	6	1.4	107	2	09X800	09X800 streptomyce
244	6	1.4	62	8	048311	048311 polioptilla	317	6	1.4	107	2	09PAQ9	09PAQ9 xylella fas
245	6	1.4	62	8	048368	048368 polioptilla	318	6	1.4	108	5	09U3X6	09U3X6 mamestra br
246	6	1.4	62	9	038618	038618 xanthomonas	319	6	1.4	108	5	09NG94	09NG94 mamestra br
247	6	1.4	62	9	038073	038073 bacterioph	320	6	1.4	110	2	069654	069654 mycobacteri
248	6	1.4	63	5	09NDAS	09NDAS bacterioph	321	6	1.4	110	2	09KZB9	09KZB9 streptomyce
249	6	1.4	63	5	09NDAS	09NDAS conus texti	322	6	1.4	110	14	09PXP9	09PXP9 human immun
250	6	1.4	63	5	09NDAS	09NDAS conus texti	323	6	1.4	112	13	09PTJ0	09PTJ0 stenococcus
251	6	1.4	64	5	09NM44	09NM44 leishmania	324	6	1.4	113	2	09WMK7	09WMK7 synchococc
252	6	1.4	65	5	09W5R0	09W5R0 drosophila	325	6	1.4	113	5	09VZ24	09VZ24 drosophila
253	6	1.4	68	2	09L3P1	09L3P1 uncultured	326	6	1.4	113	14	09YMP0	09YMP0 lymantria d
254	6	1.4	68	5	09WP19	09WP19 drosophila	327	6	1.4	114	2	045237	045237 bradyrhizob
255	6	1.4	69	5	061716	061716 anopheles g	328	6	1.4	114	11	09MVA9	09MVA9 ratiu norv
256	6	1.4	69	5	09UA97	09UA97 conus livid	329	6	1.4	115	2	09XAI3	09XAI3 streptomyce
257	6	1.4	71	14	09QAN7	09QAN7 human herpe	330	6	1.4	115	11	09RI39	09RI39 spermophilu
258	6	1.4	72	1	09UGZ5	09UGZ5 pyrococcus	331	6	1.4	115	14	085200	085200 potato viru
259	6	1.4	72	5	09UAA2	09UAA2 conus livid	332	6	1.4	115	14	09QCP5	09QCP5 potato viru
260	6	1.4	72	5	09UAA2	09UAA2 conus livid	333	6	1.4	117	1	058897	058897 pyrococcus
261	6	1.4	73	8	09MTL5	09MTL5 human immun	334	6	1.4	117	1	09VZM0	09VZM0 halobacteri
262	6	1.4	74	14	069106	069106 oenothera h	335	6	1.4	117	2	09LOZ7	09LOZ7 streptomyce
263	6	1.4	75	2	049667	049667 herpes simp	336	6	1.4	117	2	09LGA2	09LGA2 oryza sativ
264	6	1.4	75	8	09TKU9	09TKU9 mycobacteri	337	6	1.4	118	5	09N1P8	09N1P8 trypanosoma
265	6	1.4	75	14	09P112	09P112 saguaro cac	338	6	1.4	119	5	069920	069920 streptomyce
266	6	1.4	78	2	09K041	09K041 vibrio chol	339	6	1.4	119	5	09N6G3	09N6G3 trypanosoma
267	6	1.4	78	5	020607	020607 caenorhabd	340	6	1.4	119	10	043548	043548 malus domes
268	6	1.4	79	2	09RK06	09RK06 streptomyce	341	6	1.4	119	10	09M1A3	09M1A3 arbidopsi
269	6	1.4	80	2	09S350	09S350 prevotella	342	6	1.4	120	2	085650	085650 streptomyce
270	6	1.4	81	14	079297	079297 human immun	343	6	1.4	120	2	09JPM1	09JPM1 bacillus ha
271	6	1.4	82	14	098215	098215 molluscum c	344	6	1.4	120	5	09N1O7	09N1O7 trypanosoma
272	6	1.4	83	14	09J7M9	09J7M9 tt virus	345	6	1.4	120	5	09N1O0	09N1O0 trypanosoma
273	6	1.4	84	2	007503	007503 borrelia ga	346	6	1.4	120	10	049795	049795 arbidopsi
274	6	1.4	84	2	09S120	09S120 mycobacteri	347	6	1.4	121	6	018952	018952 bos taurus
275	6	1.4	85	2	097155	097155 escherichia	348	6	1.4	122	2	09KJ69	09KJ69 rhizobium l
276	6	1.4	86	14	09QST6	09QST6 human immun	349	6	1.4	124	2	008312	008312 desulfovibr
277	6	1.4	87	2	09PDB8	09PDB8 xylella fas	350	6	1.4	124	2	032547	032547 escherichia
278	6	1.4	89	5	09N1P9	09N1P9 trypanosoma	351	6	1.4	124	14	096617	096617 human immun
279	6	1.4	90	5	016596	016596 caenorhabd	352	6	1.4	125	1	074041	074041 cenarchaeum
280	6	1.4	90	14	069693	069693 human immun	353	6	1.4	125	1	074064	074064 cenarchaeum
281	6	1.4	91	2	09RXH2	09RXH2 delnoco	354	6	1.4	125	2	09P132	09P132 campylobact
282	6	1.4	91	5	09NEN2	09NEN2 caenorhabd	355	6	1.4	125	2	09R1S6	09R1S6 streptomyce
283	6	1.4	92	10	09LV87	09LV87 arabidopsi	356	6	1.4	126	2	09RXX0	09RXX0 delnoco
284	6	1.4	92	11	09Z239	09Z239 mus muscul	357	6	1.4	126	2	09Z8M1	09Z8M1 chlamydia p
285	6	1.4	93	14	097280	097280 human immun	358	6	1.4	126	2	09JSH5	09JSH5 chlamydia p
286	6	1.4	97	5	09NLP8	09NLP8 leishmania	359	6	1.4	126	14	09J1K5	09J1K5 hepaticis c
287	6	1.4	99	4	09U0J3	09U0J3 schizosacch	360	6	1.4	127	5	016914	016914 anopheles a
288	6	1.4	99	14	09U0J3	09U0J3 homo sapien	361	6	1.4	128	13	09I9H0	09I9H0 gallus gall
289	6	1.4	99	14	09U0J3	09U0J3 homo sapien	362	6	1.4	129	2	053520	053520 mycobacteri
290	6	1.4	100	2	074472	074472 salmireline	363	6	1.4	130	2	09N328	09N328 synchocyst
291	6	1.4	100	2	055567	055567 synchocyst	364	6	1.4	130	5	09N351	09N351 caenorhabd
292	6	1.4	100	5	09W4O5	09W4O5 drosophila	365	6	1.4	131	2	051403	051403 pseudomonas
293	6	1.4	101	2	030897	030897 salmireline	366	6	1.4	131	5	09VE90	09VE90 drosophila
294	6	1.4	101	5	09NBM4	09NBM4 thermomyzon	367	6	1.4	132	4	09NVC1	09NVC1 homo sapien
295	6	1.4	101	14	091083	091083 human immun	368	6	1.4	132	5	09VOT9	09VOT9 drosophila
296	6	1.4	101	14	091V80	091V80 human immun	369	6	1.4	132	5	09N1O3	09N1O3 trypanosoma
297	6	1.4	102	1	09TEC8	09TEC8 aeropyrum p	370	6	1.4	133	2	09X8Q2	09X8Q2 streptomyce
298	6	1.4	102	1	09TEC8	09TEC8 aeropyrum p	371	6	1.4	133	2	09X8Q2	09X8Q2 streptomyce
299	6	1.4	102	2	09RX94	09RX94 delnoco	372	6	1.4	133	4	09NS12	09NS12 mycobacteri
300	6	1.4	102	4	09Y421	09Y421 homo sapien	373	6	1.4	134	5	016595	016595 caenorhabd
301	6	1.4	102	10	09LIY2	09LIY2 oryza sativ	374	6	1.4	135	8	036056	036056 taeniolrhiz
302	6	1.4	102	14	091DV5	091DV5 human immun	375	6	1.4	136	5	09MZW0	09MZW0 sus scrofa
303	6	1.4	103	1	09YFT6	09YFT6 aeropyrum p	376	6	1.4	137	5	09N1O4	09N1O4 trypanosoma
304	6	1.4	103	5	09N1O9	09N1O9 trypanosoma	377	6	1.4	137	2	068053	068053 rhodobacter
305	6	1.4	103	5	09N1O8	09N1O8 trypanosoma	378	6	1.4	139	2	083766	083766 treponema p
306	6	1.4	103	5	09N1O5	09N1O5 trypanosoma	379	6	1.4	142	2	09KWC3	09KWC3 streptococ
307	6	1.4	103	10	041811	041811 zea mays (m	380	6	1.4	142	5	09XV19	09XV19 caenorhabd
308	6	1.4	104	9	021876	021876 bacterioph	381	6	1.4	142	11	09UJ93	09UJ93 mus muscul
309	6	1.4	104	9	037864	037864 bacterioph	382	6	1.4	143	1	058831	058831 pyrococcus
310	6	1.4	104	10	09JGC8	09JGC8 oryza sativ	383	6	1.4	143	4	09N289	09N289 homo sapien
311	6	1.4	105	2	025167	025167 helicobacte	384	6	1.4	144	13	093465	093465 ambystoma m

385	6	1.4	146	1	Q9Y9H4	Q9Y9H4 aeropyrum p	458	6	1.4	166	9	080149	080149 bacterioph
386	6	1.4	146	2	Q9XAA2	Q9XAA2 streptomyce	459	6	1.4	166	10	Q39544	Q39544 clivia mini
387	6	1.4	146	2	Q9JMN7	Q9JMN7 wolbachia s	460	6	1.4	166	11	008731	008731 rattus norv
388	6	1.4	146	10	Q23690	Q23690 arabidopsis	461	6	1.4	166	14	Q90510	Q90510 leishmania
389	6	1.4	148	2	Q49876	Q49876 mycobacteri	462	6	1.4	168	5	097194	097194 leishmania
390	6	1.4	148	2	Q33392	Q33392 neisseria m	463	6	1.4	169	2	087075	087075 vibrio chol
391	6	1.4	148	2	Q9S355	Q9S355 pseudomonas	464	6	1.4	169	2	09S2T1	09S2T1 streptomyce
392	6	1.4	148	5	P91814	P91814 toxocara ca	465	6	1.4	169	2	Q9KZ25	Q9KZ25 streptomyce
393	6	1.4	149	2	Q9S1V7	Q9S1V7 streptomyce	466	6	1.4	169	10	Q39342	Q39342 clivia mini
394	6	1.4	149	5	Q9V8D1	Q9V8D1 drosophila	467	6	1.4	171	2	Q33220	Q33220 rhodobacter
395	6	1.4	150	2	Q9RLX1	Q9RLX1 klebsiella	468	6	1.4	172	8	Q9MHW4	Q9MHW4 loxia curvi
396	6	1.4	150	10	Q81311	Q81311 arabidopsis	469	6	1.4	172	8	Q9MHW2	Q9MHW2 loxia curvi
397	6	1.4	150	10	Q9LZY6	Q9LZY6 arabidopsis	470	6	1.4	172	8	Q9MHW2	Q9MHW2 loxia curvi
398	6	1.4	151	1	Q9Y1V3	Q9Y1V3 mycobacteri	471	6	1.4	172	8	Q9MHW2	Q9MHW2 loxia curvi
399	6	1.4	151	2	Q53528	Q53528 caenorhabd	472	6	1.4	172	8	Q9MHW2	Q9MHW2 loxia curvi
400	6	1.4	151	5	Q23522	Q23522 caenorhabd	473	6	1.4	172	8	Q9MHW2	Q9MHW2 loxia curvi
401	6	1.4	151	10	Q9SLR4	Q9SLR4 arabidopsis	474	6	1.4	172	8	Q9MHW2	Q9MHW2 loxia curvi
402	6	1.4	153	10	Q9M2J3	Q9M2J3 arabidopsis	475	6	1.4	172	8	Q9MHW2	Q9MHW2 loxia curvi
403	6	1.4	154	1	Q29246	Q29246 archaeoglob	476	6	1.4	174	1	Q9YF05	Q9YF05 aeropyrum p
404	6	1.4	154	2	P94572	P94572 bacillus su	477	6	1.4	175	10	Q9XET4	Q9XET4 oryza sativ
405	6	1.4	154	2	Q47394	Q47394 escherichia	478	6	1.4	175	10	Q9SMT2	Q9SMT2 arabidopsis
406	6	1.4	154	2	Q9RISO	Q9RISO salmoneila	479	6	1.4	175	10	Q9WV79	Q9WV79 rattus norv
407	6	1.4	154	4	Q9UKQ3	Q9UKQ3 homo sapien	480	6	1.4	176	5	Q96357	Q96357 hyphantria
408	6	1.4	154	10	Q82010	Q82010 lycopersico	481	6	1.4	176	5	Q9W549	Q9W549 drosophila
409	6	1.4	154	10	Q82011	Q82011 lycopersico	482	6	1.4	177	5	Q22163	Q22163 caenorhabd
410	6	1.4	154	10	Q82012	Q82012 lycopersico	483	6	1.4	178	2	Q9RME0	Q9RME0 acinetobact
411	6	1.4	154	10	Q9SYV0	Q9SYV0 lycopersico	484	6	1.4	178	5	Q9RME0	Q9RME0 acinetobact
412	6	1.4	154	10	Q9SYU9	Q9SYU9 lycopersico	485	6	1.4	178	5	Q9RME0	Q9RME0 acinetobact
413	6	1.4	154	10	Q9SYU8	Q9SYU8 lycopersico	486	6	1.4	180	2	Q51735	Q51735 pseudomonas
414	6	1.4	155	2	Q9Z4V6	Q9Z4V6 salmoneila	487	6	1.4	180	10	Q9STR4	Q9STR4 arabidopsis
415	6	1.4	155	2	Q9RIR9	Q9RIR9 salmoneila	488	6	1.4	181	2	Q9XSA2	Q9XSA2 treponema d
416	6	1.4	155	2	Q9RIR7	Q9RIR7 salmoneila	489	6	1.4	181	2	Q005816	Q005816 mycobacteri
417	6	1.4	155	3	Q005863	Q005863 saccharomyc	490	6	1.4	181	10	Q9SZ43	Q9SZ43 arabidopsis
418	6	1.4	156	2	Q56118	Q56118 salmoneila	491	6	1.4	181	10	Q9LGF0	Q9LGF0 oryza sativ
419	6	1.4	156	2	Q9RLX2	Q9RLX2 klebsiella	492	6	1.4	182	4	Q14548	Q14548 homo sapien
420	6	1.4	156	2	Q9L5F3	Q9L5F3 salmoneila	493	6	1.4	182	14	Q98324	Q98324 molluscum c
421	6	1.4	156	2	P87274	P87274 saccharomyc	494	6	1.4	184	4	Q16713	Q16713 homo sapien
422	6	1.4	157	10	Q9LX72	Q9LX72 arabidopsis	495	6	1.4	184	5	Q9N7A0	Q9N7A0 leishmania
423	6	1.4	157	8	Q9WEC9	Q9WEC9 drosophila	496	6	1.4	185	1	Q9UY99	Q9UY99 pyrococcus
424	6	1.4	157	10	Q22531	Q22531 taenia pisi	497	6	1.4	185	10	Q9XFN9	Q9XFN9 arabidopsis
425	6	1.4	157	2	Q9Z647	Q9Z647 pantoea cit	498	6	1.4	185	10	Q9SUD5	Q9SUD5 arabidopsis
426	6	1.4	158	2	Q9Z647	Q9Z647 pantoea cit	499	6	1.4	186	10	Q65755	Q65755 cicler ariet
427	6	1.4	158	2	Q9Z647	Q9Z647 pantoea cit	500	6	1.4	187	3	Q9P3T4	Q9P3T4 neurospora
428	6	1.4	158	2	Q9Z647	Q9Z647 pantoea cit	501	6	1.4	187	10	Q9LXJ6	Q9LXJ6 arabidopsis
429	6	1.4	158	2	Q9RIL9	Q9RIL9 salmoneila	502	6	1.4	188	10	Q9SMT14	Q9SMT14 brassica ca
430	6	1.4	158	2	Q9RBS0	Q9RBS0 citrobacter	503	6	1.4	190	2	P84222	P84222 borrelia bu
431	6	1.4	158	2	Q9JTY91	Q9JTY91 neisseria m	504	6	1.4	190	11	Q63127	Q63127 rattus norv
432	6	1.4	158	6	Q9M089	Q9M089 macaca fasc	505	6	1.4	191	2	Q9P8X8	Q9P8X8 xylella fas
433	6	1.4	158	10	Q9SS77	Q9SS77 matricaria	506	6	1.4	191	2	Q9P8X8	Q9P8X8 xylella fas
434	6	1.4	159	2	Q9Z506	Q9Z506 citrobacter	507	6	1.4	192	2	Q66846	Q66846 aquifex aeo
435	6	1.4	159	2	Q9RM74	Q9RM74 citrobacter	508	6	1.4	192	2	Q9Z5F6	Q9Z5F6 morangella
436	6	1.4	159	2	Q9RM50	Q9RM50 escherichia	509	6	1.4	194	2	P74432	P74432 synechocyst
437	6	1.4	159	2	Q9RBS1	Q9RBS1 citrobacter	510	6	1.4	195	2	Q9RBS2	Q9RBS2 streptomyce
438	6	1.4	159	2	Q9PEE3	Q9PEE3 xylella fas	511	6	1.4	195	4	Q9NRS8	Q9NRS8 homo sapien
439	6	1.4	159	5	Q9U041	Q9U041 giardia lam	512	6	1.4	195	5	Q76887	Q76887 drosophila
440	6	1.4	159	10	Q40510	Q40510 nicotiana t	513	6	1.4	196	10	Q9SW63	Q9SW63 arabidopsis
441	6	1.4	159	10	Q40510	Q40510 nicotiana t	514	6	1.4	197	5	Q9N2V8	Q9N2V8 archaeoglob
442	6	1.4	160	2	Q44831	Q44831 borrelia bu	515	6	1.4	197	10	Q9ZVL1	Q9ZVL1 caenorhabd
443	6	1.4	160	2	Q9Z505	Q9Z505 citrobacter	516	6	1.4	197	10	Q9ZVL1	Q9ZVL1 caenorhabd
444	6	1.4	160	2	Q9RLX3	Q9RLX3 klebsiella	517	6	1.4	199	11	Q9QVW9	Q9QVW9 rattus sp.
445	6	1.4	161	2	Q9Z506	Q9Z506 klebsiella	518	6	1.4	199	13	Q9PRE4	Q9PRE4 brachydanio
446	6	1.4	161	2	Q9RLX0	Q9RLX0 klebsiella	519	6	1.4	200	2	Q9JVB8	Q9JVB8 neisseria m
447	6	1.4	161	2	Q9RLX0	Q9RLX0 klebsiella	520	6	1.4	200	5	Q9VE11	Q9VE11 drosophila
448	6	1.4	161	2	Q9RLX0	Q9RLX0 klebsiella	521	6	1.4	200	5	Q9VE11	Q9VE11 drosophila
449	6	1.4	162	2	Q9Z5F0	Q9Z5F0 proteus mir	522	6	1.4	200	10	Q65769	Q65769 craterostig
450	6	1.4	162	4	Q9S711	Q9S711 homo sapien	523	6	1.4	201	2	Q9RMX9	Q9RMX9 delnoccocus
451	6	1.4	162	13	Q9YH77	Q9YH77 lampetra fl	524	6	1.4	201	2	Q9K857	Q9K857 bacillus ha
452	6	1.4	163	2	Q47698	Q47698 escherichia	525	6	1.4	202	1	Q51967	Q51967 halobacteri
453	6	1.4	163	5	Q23014	Q23014 caenorhabd	526	6	1.4	202	2	Q9P1R1	Q9P1R1 campylobact
454	6	1.4	165	2	Q9Z5L2	Q9Z5L2 klebsiella	527	6	1.4	202	4	Q9NMK7	Q9NMK7 homo sapien
455	6	1.4	165	14	Q9YUR5	Q9YUR5 hemorrhagic	528	6	1.4	203	1	Q29208	Q29208 archaeoglob
456	6	1.4	166	2	Q9RLM6	Q9RLM6 klebsiella	529	6	1.4	203	2	Q9X840	Q9X840 streptomyce
457	6	1.4	166	5	Q9VL36	Q9VL36 drosophila	530	6	1.4	203	4	Q9NX04	Q9NX04 homo sapien

531	6	1.4	204	6	09XSH2	09xsh2 tupala glis	604	6	1.4	220	2	09KR87	09KR87 mycobacteri
532	6	1.4	204	14	075141	075141 human immun	605	6	1.4	220	10	09SUV8	09SUV8 arabisidps
533	6	1.4	204	14	075142	075142 human immun	606	6	1.4	221	3	09DW17	09DW17 aureobasidi
534	6	1.4	205	5	09VAC2	09VAC2 drosophila	607	6	1.4	221	13	09YR96	09YR96 paracaltichy
535	6	1.4	206	2	067672	067672 aquifex aeo	608	6	1.4	222	2	054191	054191 streptomyce
536	6	1.4	206	5	09V328	09V328 drosophila	609	6	1.4	222	10	09LSA8	09LSA8 arabisidps
537	6	1.4	206	8	063844	063844 hemilampyrop	610	6	1.4	222	11	061073	061073 mus musculu
538	6	1.4	207	2	032813	032813 lactococcus	611	6	1.4	223	2	09K1B2	09K1B2 neisseria m
539	6	1.4	207	2	09JYR6	09JYR6 neisseria m	612	6	1.4	223	2	09JX90	09JX90 neisseria m
540	6	1.4	207	2	09JYR7	09JYR7 neisseria m	613	6	1.4	224	2	031041	031041 salmonella
541	6	1.4	207	5	09W1F0	09W1F0 drosophila	614	6	1.4	224	2	059471	059471 klebsiella
542	6	1.4	207	2	09L126	09L126 streptomyce	615	6	1.4	224	4	094796	094796 homo sapien
543	6	1.4	208	10	041230	041230 nicotiana t	616	6	1.4	224	4	09Y4C3	09Y4C3 homo sapien
544	6	1.4	208	14	09YUF8	09YUF8 rhesus cyto	617	6	1.4	224	4	09UBT3	09UBT3 homo sapien
545	6	1.4	209	2	049583	049583 borrelia ga	618	6	1.4	224	5	09VQF8	09VQF8 drosophila
546	6	1.4	209	10	039488	039488 colocasia e	619	6	1.4	224	10	09ZVC6	09ZVC6 arabisidps
547	6	1.4	209	10	042412	042412 nicotiana s	620	6	1.4	224	14	09YR79	09YR79 hibiscus ch
548	6	1.4	210	2	09PE06	09PE06 xylella fas	621	6	1.4	225	14	09J019	09J019 lysavirus
549	6	1.4	210	5	016222	016222 caenorhabdi	622	6	1.4	226	2	052425	052425 pseudomonas
550	6	1.4	210	5	09XYB2	09XYB2 plasmodium	623	6	1.4	226	10	09S8F8	09S8F8 arabisidps
551	6	1.4	210	14	087985	087985 chimpanzee	624	6	1.4	226	14	09JEU0	09JEU0 european ba
552	6	1.4	210	14	087986	087986 chimpanzee	625	6	1.4	226	14	09JEU9	09JEU9 european ba
553	6	1.4	210	14	087987	087987 chimpanzee	626	6	1.4	226	14	09JET8	09JET8 european ba
554	6	1.4	210	14	087988	087988 chimpanzee	627	6	1.4	226	14	09JET7	09JET7 european ba
555	6	1.4	210	14	087989	087989 chimpanzee	628	6	1.4	226	14	09JET6	09JET6 european ba
556	6	1.4	211	4	087990	087990 chimpanzee	629	6	1.4	227	2	031622	031622 bacillus su
557	6	1.4	211	4	09UNAT	09unat homo sapien	630	6	1.4	227	2	007832	007832 pseudomonas
558	6	1.4	211	10	041231	041231 nicotiana t	631	6	1.4	227	4	013445	013445 homo sapien
559	6	1.4	211	14	087992	087992 chimpanzee	632	6	1.4	227	11	09WU32	09WU32 mus musculu
560	6	1.4	211	14	087994	087994 chimpanzee	633	6	1.4	229	2	09WYW3	09WYW3 thermotoga
561	6	1.4	211	14	087995	087995 chimpanzee	634	6	1.4	229	10	024002	024002 hordeum vul
562	6	1.4	211	14	087997	087997 chimpanzee	635	6	1.4	229	14	09YXAS	09YXAS bluetongue
563	6	1.4	211	14	087998	087998 chimpanzee	636	6	1.4	229	14	09WN14	09WN14 mucosal dis
564	6	1.4	211	14	087996	087996 chimpanzee	637	6	1.4	229	14	09WN12	09WN12 mucosal dis
565	6	1.4	211	14	087997	087997 chimpanzee	638	6	1.4	229	14	09WN11	09WN11 mucosal dis
566	6	1.4	211	14	087993	087993 chimpanzee	639	6	1.4	229	14	09WN10	09WN10 mucosal dis
567	6	1.4	211	14	087996	087996 chimpanzee	640	6	1.4	229	14	09WN09	09WN09 mucosal dis
568	6	1.4	212	2	09JYH3	09jyh3 neisseria m	641	6	1.4	229	14	09WN08	09WN08 mucosal dis
569	6	1.4	212	2	09SEY8	09sef8 arabisidps	642	6	1.4	229	14	09WN07	09WN07 mucosal dis
570	6	1.4	213	2	030553	030553 helicobacte	643	6	1.4	229	14	09WN06	09WN06 mucosal dis
571	6	1.4	213	5	076855	076855 dictyostell	644	6	1.4	229	14	09WN05	09WN05 mucosal dis
572	6	1.4	213	14	087999	087999 chimpanzee	645	6	1.4	229	14	09WN04	09WN04 mucosal dis
573	6	1.4	214	5	P91050	P91050 caenorhabdi	646	6	1.4	229	14	09WN03	09WN03 mucosal dis
574	6	1.4	214	8	095933	095933 phascosolom	647	6	1.4	229	14	09WN02	09WN02 mucosal dis
575	6	1.4	214	10	09M4C6	09M4C6 avena fatua	648	6	1.4	229	14	09WN00	09WN00 mucosal dis
576	6	1.4	215	2	026097	026097 helicobacte	649	6	1.4	229	14	09W9L3	09W9L3 mucosal dis
577	6	1.4	215	2	P72739	P72739 synechocyst	650	6	1.4	229	14	09W9L3	09W9L3 mucosal dis
578	6	1.4	215	5	09N5B2	09N5B2 helicobacte	651	6	1.4	229	14	09W9E2	09W9E2 mucosal dis
579	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	652	6	1.4	229	14	09W8P1	09W8P1 mucosal dis
580	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	653	6	1.4	229	14	09W874	09W874 mucosal dis
581	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	654	6	1.4	230	5	019871	019871 caenorhabdi
582	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	655	6	1.4	230	10	022906	022906 arabisidps
583	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	656	6	1.4	230	10	09LETO	09LETO arabisidps
584	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	657	6	1.4	231	3	09UT94	09UT94 schizosacch
585	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	658	6	1.4	231	4	09Y2P3	09Y2P3 homo sapien
586	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	659	6	1.4	231	11	054872	054872 ratius norv
587	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	660	6	1.4	232	8	09TBM1	09TBM1 acropora te
588	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	661	6	1.4	232	8	051759	051759 pseudomonas
589	6	1.4	215	8	09N5B2	09N5B2 caenorhabdi	662	6	1.4	233	2	051759	051759 pseudomonas
590	6	1.4	216	2	09RKV9	09RKV9 streptomyce	663	6	1.4	235	2	085219	085219 photobacter
591	6	1.4	216	2	09RCM6	09RCM6 streptomyce	664	6	1.4	235	10	09LRF3	09LRF3 oryza sativ
592	6	1.4	216	4	043880	043880 homo sapien	665	6	1.4	235	11	063068	063068 ratius norv
593	6	1.4	216	6	09N202	09N202 callitrix	666	6	1.4	235	14	P87580	P87580 cydia pomon
594	6	1.4	216	14	09NLP3	09NLP3 bluetongue	667	6	1.4	236	10	096491	096491 forsythia x
595	6	1.4	217	1	027742	027742 methanobact	668	6	1.4	236	10	09LIW6	09LIW6 oryza sativ
596	6	1.4	217	2	045216	045216 bradyrhizob	669	6	1.4	237	5	P96924	P96924 mycobacteri
597	6	1.4	217	2	067290	067290 aquifex aeo	670	6	1.4	237	5	09N8U0	09N8U0 trypanosoma
598	6	1.4	217	2	09S1E3	09S1E3 wolinnella s	671	6	1.4	237	14	066623	066623 equine herp
599	6	1.4	217	10	09SC40	09SC40 pisum sativ	672	6	1.4	238	2	066159	066159 streptomyce
600	6	1.4	218	10	09LS09	09LS09 arabisidps	673	6	1.4	238	2	085927	085927 sphingomona
601	6	1.4	219	8	09Z215	09Z215 cyclotheuthi	674	6	1.4	238	2	09L8G3	09L8G3 mycoplasma
602	6	1.4	220	2	P72807	P72807 synechocyst	675	6	1.4	238	11	09JULO	09JULO mus musculu
603	6	1.4	220	2	P72807	P72807 synechocyst	676	6	1.4	238	14	090146	090146 macaca mula

677	6	1.4	239	2	Q9RPX7	Q9RPX7 brucella su	750	6	1.4	262	10	080680	080680 arabisdopsis
678	6	1.4	240	5	Q9VSD8	Q9VSD8 drosophila	751	6	1.4	263	2	086931	086931 salmonella
679	6	1.4	241	2	Q9RSX2	Q9RSX2 delnecoccus	752	6	1.4	263	2	000815	000815 plasmod r46
680	6	1.4	241	2	Q9K3V2	Q9K3V2 streptomyces	753	6	1.4	263	2	09S5E7	09S5E7 streptomyces
681	6	1.4	241	10	Q9XFF30	Q9XFF30 oryza sativ	754	6	1.4	263	2	09RM43	09RM43 escherichia
682	6	1.4	242	1	057761	057761 pyrococcus	755	6	1.4	263	2	09R1L5	09R1L5 salmonella
683	6	1.4	242	10	Q43565	Q43565 narsicissus p	756	6	1.4	263	2	09KRV21	09KRV21 acinetobact
684	6	1.4	242	14	Q9Q916	Q9Q916 rabbit fibr	757	6	1.4	263	7	078027	078027 mus musculu
685	6	1.4	242	14	Q9O8P1	Q9O8P1 myxoma viru	758	6	1.4	264	2	050552	050552 thermus agu
686	6	1.4	244	11	Q92202	Q92202 mus musculu	759	6	1.4	264	2	09Z4N1	09Z4N1 streptomyces
687	6	1.4	244	11	Q9WU31	Q9WU31 mus musculu	760	6	1.4	264	2	09K8H9	09K8H9 bacillus ha
688	6	1.4	244	11	Q9J150	Q9J150 mus musculu	761	6	1.4	264	10	Q9M4X6	Q9M4X6 oryza sativ
689	6	1.4	245	4	Q9PMF6	Q9PMF6 campylobact	762	6	1.4	265	3	093841	093841 colilectric
690	6	1.4	245	4	Q9NPD3	Q9NPD3 homo sapien	763	6	1.4	265	4	09NRG2	09NRG2 homo sapien
691	6	1.4	246	5	Q9VEX8	Q9VEX8 drosophila	764	6	1.4	265	5	P90819	P90819 cenorchabdi
692	6	1.4	246	10	Q9LF75	Q9LF75 arabisdopsis	765	6	1.4	265	10	Q93598	Q93598 chlamydomon
693	6	1.4	246	10	Q9LE13	Q9LE13 arabisdopsis	766	6	1.4	265	10	Q9LE13	Q9LE13 hordeum vul
694	6	1.4	247	2	Q9JPC9	Q9JPC9 rhodocycilus	767	6	1.4	265	14	P88825	P88825 salmireline
695	6	1.4	247	14	P89073	P89073 rabies viru	768	6	1.4	266	11	Q9JHV1	Q9JHV1 mus musculu
696	6	1.4	248	10	Q9LF74	Q9LF74 arabisdopsis	769	6	1.4	267	2	030473	030473 bacillus su
697	6	1.4	248	11	Q9R273	Q9R273 rattus norv	770	6	1.4	267	2	09WXX7	09WXX7 thermotoga
698	6	1.4	249	2	Q9S4Y4	Q9S4Y4 yersinia en	771	6	1.4	268	2	033704	033704 streptococc
699	6	1.4	249	4	Q43508	Q43508 homo sapien	772	6	1.4	268	5	Q9MAX7	Q9MAX7 dictyosteli
700	6	1.4	249	6	Q9N216	Q9N216 felis silve	773	6	1.4	269	2	P71540	P71540 mycobacteri
701	6	1.4	249	8	Q9MTJ8	Q9MTJ8 oenothera h	774	6	1.4	269	2	Q9XAC7	Q9XAC7 streptomyces
702	6	1.4	249	10	Q39823	Q39823 glycine max	775	6	1.4	269	2	Q9S2U6	Q9S2U6 streptomyces
703	6	1.4	250	2	Q87659	Q87659 salmoneila	776	6	1.4	269	10	Q9MIB5	Q9MIB5 arabisdopsis
704	6	1.4	250	2	Q9ZAK1	Q9ZAK1 streptomyces	777	6	1.4	270	1	Q92925	Q92925 archaeoglob
705	6	1.4	250	2	Q9RLR5	Q9RLR5 legionella	778	6	1.4	270	2	Q95994	Q95994 synecocyst
706	6	1.4	250	6	Q9N215	Q9N215 felis silve	779	6	1.4	270	2	Q9RRY3	Q9RRY3 delnecoccus
707	6	1.4	250	10	Q9M0V5	Q9M0V5 arabisdopsis	780	6	1.4	271	2	Q9X470	Q9X470 streptomyces
708	6	1.4	252	6	Q9XS81	Q9XS81 sus scrofa	781	6	1.4	271	2	Q9S2V8	Q9S2V8 streptomyces
709	6	1.4	252	6	Q9TV88	Q9TV88 sus scrofa	782	6	1.4	272	2	Q9Z510	Q9Z510 klebsiella
710	6	1.4	252	6	Q9TV87	Q9TV87 sus scrofa	783	6	1.4	272	5	017954	017954 cenorchabdi
711	6	1.4	252	6	Q9TV86	Q9TV86 sus scrofa	784	6	1.4	273	5	Q34866	Q34866 bacillus su
712	6	1.4	253	1	Q9YCK2	Q9YCK2 aeropyrum p	785	6	1.4	273	10	Q9YD09	Q9YD09 drosophila
713	6	1.4	253	2	Q9L6M8	Q9L6M8 salmoneila	786	6	1.4	273	10	Q22400	Q22400 arabisdopsis
714	6	1.4	253	10	Q80674	Q80674 arabisdopsis	787	6	1.4	273	10	Q08935	Q08935 nicotiana s
715	6	1.4	254	5	Q9XAK4	Q9XAK4 streptomyces	788	6	1.4	274	1	Q28585	Q28585 archaeoglob
716	6	1.4	254	5	Q22644	Q22644 cenorchabdi	789	6	1.4	274	2	Q9X558	Q9X558 streptomyces
717	6	1.4	255	2	Q84691	Q84691 chlamydia t	790	6	1.4	274	11	Q64369	Q64369 mus musculu
718	6	1.4	255	2	Q9ZM06	Q9ZM06 helicobacte	791	6	1.4	275	2	Q92633	Q92633 listeria mo
719	6	1.4	255	2	Q9PLP2	Q9PLP2 chlamydia m	792	6	1.4	275	10	Q81655	Q81655 hemerocall
720	6	1.4	255	5	Q18404	Q18404 drosophila	793	6	1.4	276	1	Q27615	Q27615 methanobact
721	6	1.4	256	2	Q9KS35	Q9KS35 vibrio chol	794	6	1.4	276	5	Q9PC59	Q9PC59 xyella fas
722	6	1.4	256	2	Q9KAS9	Q9KAS9 bacillus ha	795	6	1.4	276	5	Q9V4P0	Q9V4P0 drosophila
723	6	1.4	256	3	P79012	P79012 schizosacch	796	6	1.4	277	2	Q9RG33	Q9RG33 lactobacill
724	6	1.4	256	5	Q17978	Q17978 cenorchabdi	797	6	1.4	277	5	Q9XZY1	Q9XZY1 leishmania
725	6	1.4	256	9	Q9T1Q5	Q9T1Q5 bacterioph	798	6	1.4	277	5	Q9U7L7	Q9U7L7 callobacter
726	6	1.4	256	10	Q9SGR2	Q9SGR2 arabisdopsis	799	6	1.4	277	5	Q9NUV9	Q9NUV9 penaeus sem
727	6	1.4	256	10	Q9LP75	Q9LP75 arabisdopsis	800	6	1.4	278	2	Q9RYE2	Q9RYE2 delnecoccus
728	6	1.4	257	2	Q9ZAI4	Q9ZAI4 pseudomonas	801	6	1.4	278	2	Q9RYE2	Q9RYE2 streptomyces
729	6	1.4	257	2	Q9J004	Q9J004 vibrio chol	802	6	1.4	279	5	Q18512	Q18512 cenorchabdi
730	6	1.4	257	3	Q9UTJ2	Q9UTJ2 schizosacch	803	6	1.4	280	2	Q53316	Q53316 streptomyces
731	6	1.4	257	14	Q12682	Q12682 kaposi's sa	804	6	1.4	280	4	Q9ZAE7	Q9ZAE7 burkholderi
732	6	1.4	257	14	Q40946	Q40946 kaposi's sa	805	6	1.4	280	4	Q99949	Q99949 homo sapien
733	6	1.4	257	14	Q98147	Q98147 kaposi's sa	806	6	1.4	280	8	Q9T2M1	Q9T2M1 saccharomyc
734	6	1.4	257	14	P88962	P88962 kaposi's sa	807	6	1.4	280	10	Q42446	Q42446 zea mays (m
735	6	1.4	258	2	Q9PBI4	Q9PBI4 xyella fas	808	6	1.4	280	10	Q96317	Q96317 arabisdopsis
736	6	1.4	258	2	Q9UR60	Q9UR60 neisseria m	809	6	1.4	280	11	Q35626	Q35626 mus musculu
737	6	1.4	258	14	Q56373	Q56373 sida golden	810	6	1.4	280	11	Q9JKF8	Q9JKF8 rattus norv
738	6	1.4	259	1	Q28465	Q28465 archaeoglob	811	6	1.4	280	13	Q93526	Q93526 gallus gall
739	6	1.4	259	2	Q85667	Q85667 escherichia	812	6	1.4	281	1	Q9YFS1	Q9YFS1 aeropyrum p
740	6	1.4	259	2	Q86634	Q86634 streptomyces	813	6	1.4	281	2	Q52472	Q52472 streptocall
741	6	1.4	259	4	Q9UL57	Q9UL57 homo sapien	814	6	1.4	281	2	Q9WYA7	Q9WYA7 thermotoga
742	6	1.4	259	10	Q24643	Q24643 arabisdopsis	815	6	1.4	281	4	Q9Y272	Q9Y272 homo sapien
743	6	1.4	259	11	Q08579	Q08579 mus musculu	816	6	1.4	281	4	Q9NYB4	Q9NYB4 aeropyrum p
744	6	1.4	260	2	Q69151	Q69151 photobacter	817	6	1.4	282	1	Q9YCM7	Q9YCM7 mycobacteri
745	6	1.4	260	2	Q49657	Q49657 mycobacteri	818	6	1.4	282	2	Q9RM65	Q9RM65 delnecoccus
746	6	1.4	260	2	Q9ZHX3	Q9ZHX3 brucella me	819	6	1.4	283	2	Q9Z816	Q9Z816 chlamydia p
747	6	1.4	260	2	Q9Z6F6	Q9Z6F6 vibrio para	820	6	1.4	284	2	Q9WZ08	Q9WZ08 thermotoga
748	6	1.4	260	2	Q9K080	Q9K080 vibrio chol	821	6	1.4	284	2	Q9RM51	Q9RM51 enterobacte
749	6	1.4	262	1	Q58703	Q58703 methanococc	822	6	1.4	284	2	Q9RM49	Q9RM49 enterobacte

823	6	1.4	284	2	Q9L966	Q9L966 streptomyc	896	6	1.4	305	5	Q23601	Q23601 caenorhabd1
824	6	1.4	284	9	Q01088	Q01088 bacterioph	897	6	1.4	305	10	Q9LJA0	Q9LJA0 arabidopsi
825	6	1.4	285	2	Q925C0	Q925C0 streptomyc	898	6	1.4	306	2	Q9RH78	Q9RH78 bradyrhizob
826	6	1.4	285	5	Q18853	Q18853 caenorhabd1	899	6	1.4	306	10	Q9T046	Q9T046 arabidopsi
827	6	1.4	286	2	P74318	P74318 synechocyst	900	6	1.4	307	1	Q50095	Q50095 pyrococcus
828	6	1.4	286	2	Q9ZC23	Q9ZC23 yersinia pe	901	6	1.4	307	1	Q9V0M8	Q9V0M8 pyrococcus
829	6	1.4	286	2	Q9Z5P9	Q9Z5P9 enterobacte	902	6	1.4	307	2	Q50662	Q50662 mycobacteri
830	6	1.4	286	2	Q9X7J2	Q9X7J2 enterobacte	903	6	1.4	308	4	Q9JRG2	Q9JRG2 neisseria m
831	6	1.4	286	2	Q9RM52	Q9RM52 enterobacte	904	6	1.4	308	4	Q92788	Q92788 homo sapien
832	6	1.4	286	5	Q23011	Q23011 caenorhabd1	905	6	1.4	308	11	Q88667	Q88667 mus musculu
833	6	1.4	286	5	Q9NPF3	Q9NPF3 drosophila	906	6	1.4	308	11	Q61478	Q61478 mus musculu
834	6	1.4	286	14	Q9O8V4	Q9O8V4 rabbit fibr	907	6	1.4	309	10	Q65213	Q65213 volvox cart
835	6	1.4	286	14	Q9O8H7	Q9O8H7 myxoma viru	908	6	1.4	309	10	Q22179	Q22179 arabidopsi
836	6	1.4	287	5	Q9W376	Q9W376 drosophila	909	6	1.4	310	2	Q9RSK4	Q9RSK4 delinococcu
837	6	1.4	288	4	Q9Y4U1	Q9Y4U1 homo sapien	910	6	1.4	310	5	Q76361	Q76361 caenorhabd1
838	6	1.4	289	2	Q9KZV3	Q9KZV3 streptomyc	911	6	1.4	310	6	Q9TU05	Q9TU05 sus scrofa
839	6	1.4	289	2	Q9KXK6	Q9KXK6 streptomyc	912	6	1.4	310	10	Q9ZUN4	Q9ZUN4 arabidopsi
840	6	1.4	289	10	Q39825	Q39825 glycine max	913	6	1.4	310	10	Q9LWX6	Q9LWX6 oryza saliv
841	6	1.4	290	2	Q68115	Q68115 rhodobacter	914	6	1.4	311	2	Q9ZGPI	Q9ZGPI staphylococ
842	6	1.4	290	2	Q9RJ39	Q9RJ39 streptomyc	915	6	1.4	311	2	Q9RUT5	Q9RUT5 delinococcu
843	6	1.4	290	5	Q94482	Q94482 dictyosteli	916	6	1.4	311	5	Q9N4E0	Q9N4E0 caenorhabd1
844	6	1.4	290	14	Q86876	Q86876 turkey hecp	917	6	1.4	312	2	P72457	P72457 streptomyc
845	6	1.4	290	14	Q89483	Q89483 gallid hecp	918	6	1.4	312	5	Q21373	Q21373 caenorhabd1
846	6	1.4	290	14	Q69304	Q69304 gallid hecp	919	6	1.4	313	2	Q59680	Q59680 pseudomonas
847	6	1.4	291	2	Q9S526	Q9S526 clostridium	920	6	1.4	313	2	Q53149	Q53149 mycobacteri
848	6	1.4	292	2	Q52032	Q52032 pseudomonas	921	6	1.4	313	10	Q23549	Q23549 arabidopsi
849	6	1.4	292	5	Q21771	Q21771 pseudomonas	922	6	1.4	313	14	Q56212	Q56212 hepatitis g
850	6	1.4	292	10	Q9SPB9	Q9SPB9 oryza sativ	923	6	1.4	314	2	Q30698	Q30698 helicobacte
851	6	1.4	293	2	Q05190	Q05190 caulobacter	924	6	1.4	314	2	Q25739	Q25739 helicobacte
852	6	1.4	293	2	Q32376	Q32376 commamonas t	925	6	1.4	314	2	Q68919	Q68919 streptomyc
853	6	1.4	293	2	Q9RW82	Q9RW82 delinococcu	926	6	1.4	314	2	Q9ZKX3	Q9ZKX3 helicobacte
854	6	1.4	293	2	Q9K5C2	Q9K5C2 burkholderi	927	6	1.4	314	5	Q96432	Q96432 trichomonas
855	6	1.4	293	4	Q14836	Q14836 homo sapien	928	6	1.4	315	2	Q55140	Q55140 synechocyst
856	6	1.4	293	5	Q9U126	Q9U126 leishmania	929	6	1.4	315	4	Q9P1Q4	Q9P1Q4 homo sapien
857	6	1.4	294	2	Q44382	Q44382 agrobacteri	930	6	1.4	315	6	Q9TUD0	Q9TUD0 pan troglod
858	6	1.4	294	10	Q9SVL2	Q9SVL2 arabidopsi	931	6	1.4	315	6	Q9TUB8	Q9TUB8 gorilla gor
859	6	1.4	294	10	Q9SM72	Q9SM72 oryza sativ	932	6	1.4	315	6	Q9TSM8	Q9TSM8 macaca fasc
860	6	1.4	295	2	Q32850	Q32850 mycobacteri	933	6	1.4	315	10	Q9SCQ1	Q9SCQ1 arabidopsi
861	6	1.4	295	2	Q9RT89	Q9RT89 delinococcu	934	6	1.4	316	10	P81392	P81392 antirrhinum
862	6	1.4	295	4	Q9NRY6	Q9NRY6 homo sapien	935	6	1.4	316	10	Q42428	Q42428 castanea sa
863	6	1.4	296	1	Q27257	Q27257 methanobact	936	6	1.4	317	2	P94680	P94680 commamonas t
864	6	1.4	296	2	Q50407	Q50407 mycobacteri	937	6	1.4	317	4	Q95024	Q95024 homo sapien
865	6	1.4	296	5	Q9XX28	Q9XX28 caenorhabd1	938	6	1.4	317	5	Q9W020	Q9W020 drosophila
866	6	1.4	296	11	Q9JIZ9	Q9JIZ9 mus musculu	939	6	1.4	317	5	Q28025	Q28025 bos taurus
867	6	1.4	297	4	Q9NSE7	Q9NSE7 homo sapien	940	6	1.4	317	6	Q77616	Q77616 canis famli
868	6	1.4	297	5	Q9VDI4	Q9VDI4 drosophila	941	6	1.4	318	2	Q9XAK3	Q9XAK3 streptomyc
869	6	1.4	298	1	Q9YAK1	Q9YAK1 aeropyrum p	942	6	1.4	318	2	Q9PER5	Q9PER5 xylella fas
870	6	1.4	298	2	Q85944	Q85944 sphingomona	943	6	1.4	318	2	Q9KCU4	Q9KCU4 leptospira
871	6	1.4	298	2	P73094	P73094 synechocyst	944	6	1.4	318	4	Q9U6F7	Q9U6F7 homo sapien
872	6	1.4	298	2	Q9K1U2	Q9K1U2 chlamydia p	945	6	1.4	319	10	Q9S137	Q9S137 arabidopsi
873	6	1.4	298	14	Q9JUT5	Q9JUT5 human immun	946	6	1.4	319	2	Q83552	Q83552 treponema p
874	6	1.4	299	2	Q9KZB6	Q9KZB6 streptomyc	947	6	1.4	319	2	Q9X7S9	Q9X7S9 streptomyc
875	6	1.4	299	2	Q9JRK1	Q9JRK1 neisseria m	948	6	1.4	319	5	Q9U2N8	Q9U2N8 caenorhabd1
876	6	1.4	299	5	Q9NEL5	Q9NEL5 leishmania	949	6	1.4	320	2	P94346	P94346 bacillus st
877	6	1.4	299	5	Q9N4U6	Q9N4U6 caenorhabd1	950	6	1.4	320	2	Q9ARR2	Q9ARR2 delinococcu
878	6	1.4	300	2	P76881	P76881 escherichia	951	6	1.4	320	5	Q20359	Q20359 caenorhabd1
879	6	1.4	300	2	Q9RYJ1	Q9RYJ1 delinococcu	952	6	1.4	321	1	Q27863	Q27863 methanobact
880	6	1.4	300	2	Q9L2H6	Q9L2H6 streptomyc	953	6	1.4	321	3	P78915	P78915 schizosacch
881	6	1.4	301	8	Q9MR12	Q9MR12 spondylus s	954	6	1.4	321	10	Q48574	Q48574 arabidopsi
882	6	1.4	301	8	Q9MR11	Q9MR11 spondylus n	955	6	1.4	321	10	Q39683	Q39683 dlanthus ca
883	6	1.4	301	14	Q9J3T3	Q9J3T3 human rotav	956	6	1.4	321	14	Q87697	Q87697 chimpanzee
884	6	1.4	302	2	Q53286	Q53286 mycobacteri	957	6	1.4	322	1	Q27145	Q27145 methanobact
885	6	1.4	302	2	Q9MM83	Q9MM83 lactococcu	958	6	1.4	322	2	Q9KZK2	Q9KZK2 streptomyc
886	6	1.4	302	5	Q9XV38	Q9XV38 caenorhabd1	959	6	1.4	322	2	Q9K497	Q9K497 streptomyc
887	6	1.4	303	5	Q9U3P7	Q9U3P7 caenorhabd1	960	6	1.4	322	5	Q9USF4	Q9USF4 entamoeba h
888	6	1.4	303	1	Q58803	Q58803 pyrococcus	961	6	1.4	323	5	Q18623	Q18623 caenorhabd1
889	6	1.4	303	11	Q88550	Q88550 rattus norv	962	6	1.4	325	2	P96379	P96379 mycobacteri
890	6	1.4	304	2	Q9PPD5	Q9PPD5 campylobact	963	6	1.4	325	10	Q9ZTK4	Q9ZTK4 vltis vinif
891	6	1.4	304	4	Q9Y4X2	Q9Y4X2 homo sapien	964	6	1.4	325	10	Q9LTV8	Q9LTV8 arabidopsi
892	6	1.4	304	5	Q96491	Q96491 plasmodium	965	6	1.4	326	4	Q9NUV1	Q9NUV1 homo sapien
893	6	1.4	304	5	Q9N303	Q9N303 caenorhabd1	966	6	1.4	326	10	Q9STU1	Q9STU1 arabidopsi
894	6	1.4	304	10	Q9M894	Q9M894 arabidopsi	967	6	1.4	326	10	Q9M9F9	Q9M9F9 arabidopsi
895	6	1.4	305	2	Q9K4D4	Q9K4D4 streptomyc	968	6	1.4	327	2	Q9ZBW4	Q9ZBW4 streptomyc

DR EMBL: AB014717; BAA3723.1; JOINED.
 DR HSSP: P19438; INCE.
 DR INTERPRO: IPR000488; -
 DR INTERPRO: IPR001368; -
 DR PRAM: PR000020; TNFR_c6; 2.
 DR PRAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 SO SEQUENCE 440 AA; 47894 MW; 7E9367DF3ED24DDE CRC64;

Query Match 84.8%; Score 373; DB 4; Length 440;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 APOKRSSPSGICPPGHHSSEDRDCISCKYGDYSTHNNDLLFCRCRCDGSEVELS 127
 DB 68 APOKRSSPSGICPPGHHSSEDRDCISCKYGDYSTHNNDLLFCRCRCDGSEVELS 127
 QY 128 PCTTRNTVCCCEGTFRFEDSPCMCKRCRTGCPRGWVKVODCTPMGSDIECVHESGTHK 187
 DB 128 PCTTRNTVCCCEGTFRFEDSPCMCKRCRTGCPRGWVKVODCTPMGSDIECVHESGTHK 187
 QY 188 SGEAPAVEETVSSPGTPASPCSLSGIIGVTAAYVLIYAVFVCKSLMKKVLPLYLKI 247
 DB 188 SGEAPAVEETVSSPGTPASPCSLSGIIGVTAAYVLIYAVFVCKSLMKKVLPLYLKI 247
 QY 248 CSGGGGPERDRSSORPGADNVLNETVSLPTQVPEQEMEVOEPAEPGVNMLSPGE 307
 DB 248 CSGGGGPERDRSSORPGADNVLNETVSLPTQVPEQEMEVOEPAEPGVNMLSPGE 307
 QY 248 CSGGGGPERDRSSORPGADNVLNETVSLPTQVPEQEMEVOEPAEPGVNMLSPGE 307
 DB 248 CSGGGGPERDRSSORPGADNVLNETVSLPTQVPEQEMEVOEPAEPGVNMLSPGE 307
 QY 308 SEHLEPAEAEERSRRRLVYANEGDPTETLRQCFDDFADLVPPDSMEPLMRKIGLMDNE 367
 DB 308 SEHLEPAEAEERSRRRLVYANEGDPTETLRQCFDDFADLVPPDSMEPLMRKIGLMDNE 367
 QY 368 IKVAKAAGHRDTLYTMLIKWVKRTGRDASVHTLLDALETIGERLAKOKIEDHLLSSGK 427
 DB 368 IKVAKAAGHRDTLYTMLIKWVKRTGRDASVHTLLDALETIGERLAKOKIEDHLLSSGK 427
 QY 428 FMYLEGNADSAMS 440
 DB 428 FMYLEGNADSAMS 440
 RESULT 3
 ID 015517 PRELIMINARY; PRT; 411 AA.
 AC 015517;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CYTOTOXIC TRAIL RECEPTOR-2.
 GN DR5 OR TRICK2A OR ZTNFR9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McFarlane M., Ahmed M., Sriivasula S.M., Fernandes,Alnemri T.,
 RA Cohen G.M., Alnemri E.S.;
 RA J. Biol. Chem. 0:0-0(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Screation G.R., Mongkolsapaya J., Xu X., Cowper A.E., McMichael A.J.,
 RA Bell A.J.;
 RA Curr. Biol. 0:0-0(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98090092; Pubmed=9430227;
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
 RT "death receptor 5, a member of the TNFR family, and DR4 induce

RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";
 RL Immunity 7:821-830(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Hood L.;
 RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;
 RT "Homo sapiens homolog of tumor necrosis factor receptor.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF020501; AAB71412.1; -
 DR EMBL: AF018657; AAB70577.1; -
 DR EMBL: AF016268; AAC01565.1; -
 DR EMBL: AF192548; AAF07175.1; -
 DR HSSP: P19438; 1EXT.
 DR INTERPRO: IPR000488; -
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_c6; 2.
 DR PRAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KW Receptor.
 SO SEQUENCE 411 AA; 45127 MW; D76A1C9B2FC747F9 CRC64;

Query Match 52.0%; Score 229; DB 4; Length 411;
 Best Local Similarity 100.0%; Pred. No. 5.1e-223;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 SGIIIGVTAAYVLIYAVFVCKSLMKKVLPLYLKGICSGGGGPERDRSSORPGADNV 271
 DB 183 SGIIIGVTAAYVLIYAVFVCKSLMKKVLPLYLKGICSGGGGPERDRSSORPGADNV 242
 QY 272 LNETVSLPTQVPEQEMEVOEPAEPGVNMLSPGESEHLEPAEAEERSRRRLVYANE 331
 DB 243 LNETVSLPTQVPEQEMEVOEPAEPGVNMLSPGESEHLEPAEAEERSRRRLVYANE 302
 QY 332 GDPETLRQCFDDFADLVPPDSMEPLMRKIGLMDNETIKVAKAAGHRDTLYTMLIKWN 391
 DB 303 GDPETLRQCFDDFADLVPPDSMEPLMRKIGLMDNETIKVAKAAGHRDTLYTMLIKWN 362
 QY 392 KTRGDASVHTLLDALETIGERLAKOKIEDHLLSSGFMYLEGNADSAMS 440
 DB 363 KTRGDASVHTLLDALETIGERLAKOKIEDHLLSSGFMYLEGNADSAMS 411

RESULT 4
 ID 015508 PRELIMINARY; PRT; 411 AA.
 AC 015508;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE P53-REGULATED DNA DAMAGE-INDUCIBLE CELL DEATH RECEPTOR (FAS-LIKE
 DE PROTEIN PRECURSOR).
 GN KILLER OR DR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue-Ovarian;
 RA Ku G.S., el-Deiry W.S.;
 RA Nat. Genet. 16:0-0(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97390508; Pubmed=9242610;
 RA Pan G., Ni J., Wei Y.F., Yu G., Gentz R., Dixit V.M.;
 RT "an antagonist decoy receptor and a death domain-containing receptor
 for TRAIL.";

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RL Science 277:815-818(1997).
RP [3]
RP SEQUENCE FROM N.A.
RA Cao X., Zhang W., Wan T.
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF022386; AAB71949.1;
DR EMBL: AF012628; AAB67109.1;
DR EMBL: AF153687; AAF75587.1;
DR HSSP: P19438; 1EXT.
DR INTERPRO: IPR000488;
DR INTERPRO: IPR001368;
DR PRAM: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 411 AA; 45083 MW; 57D50020E72CC954 CRC64;

Query Match 52.0%; Score 229; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 5, 1e-223;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 SGIIGTVAAVLIYAVFVCKSLMKKVLPLYKIGSGGGGPERVDRSSQRPAGADNV 271
DB 183 SGIIGTVAAVLIYAVFVCKSLMKKVLPLYKIGSGGGGPERVDRSSQRPAGADNV 242
QY 272 LNEIVSTILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEAEARSQRRLLVPANE 331
DB 243 LNEIVSTILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEAEARSQRRLLVPANE 302
QY 332 GDEPTLRQCFDFFADLVPPDSWEPLMRKLGIMDNEIKYAKAAGHRTLYTMLIKWVN 391
DB 303 GDEPTLRQCFDFFADLVPPDSWEPLMRKLGIMDNEIKYAKAAGHRTLYTMLIKWVN 362
QY 392 KTRGRDASVHTLDALETLGERLAKOKIEDHLSSGKFMYLEGNADSAMS 440
DB 363 KTRGRDASVHTLDALETLGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411

RESULT 5
014720 PRELIMINARY; PRT; 411 AA.
AC 014720;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE DEATH RECEPTOR 5.
GN DR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97390509; PubMed=9242611;
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA Goddard A.D., Godowski P., Ashkenazi A.;
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT receptors."
RT Science 277:818-821(1997).
DR EMBL: AF012535; AAB67103.1;
DR HSSP: P19438; 1EXT.
DR INTERPRO: IPR000488;
DR INTERPRO: IPR001368;
DR PRAM: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 411 AA; 45081 MW; 069BDD63CA608953 CRC64;

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Query Match 51.6%; Score 227; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 5, 4e-221;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 SGIIGTVAAVLIYAVFVCKSLMKKVLPLYKIGSGGGGPERVDRSSQRPAGADNV 271
DB 183 SGIIGTVAAVLIYAVFVCKSLMKKVLPLYKIGSGGGGPERVDRSSQRPAGADNV 242
QY 272 LNEIVSTILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEAEARSQRRLLVPANE 331
DB 243 LNEIVSTILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEAEARSQRRLLVPANE 302
QY 332 GDEPTLRQCFDFFADLVPPDSWEPLMRKLGIMDNEIKYAKAAGHRTLYTMLIKWVN 391
DB 303 GDEPTLRQCFDFFADLVPPDSWEPLMRKLGIMDNEIKYAKAAGHRTLYTMLIKWVN 362
QY 392 KTRGRDASVHTLDALETLGERLAKOKIEDHLSSGKFMYLEGNADSAMS 438
DB 363 KTRGRDASVHTLDALETLGERLAKOKIEDHLSSGKFMYLEGNADSAMS 409

RESULT 6
000220 PRELIMINARY; PRT; 468 AA.
ID 000220;
AC 000220;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CYTOTOXIC LIGAND TRAIL RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97238921; PubMed=9082380;
RA Pan G., O'Rourke K., Chinaiyan A.M., Gentz R., Edner R., Ni J.,
RA Dixit V.M.;
RT "The receptor for the cytotoxic ligand TRAIL."
RT Science 276:111-113(1997).
DR EMBL: U90875; AAC51226.1;
DR HSSP: P19438; 1EXT.
DR INTERPRO: IPR000488;
DR INTERPRO: IPR001368;
DR PRAM: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 468 AA; 50025 MW; 1B85DCDC2C8760F7 CRC64;

Query Match 3.6%; Score 16; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 1, 8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 DCTPWSDIQCVHKESG 184
DB 220 DCTPWSDIQCVHKESG 235

RESULT 7
09Y604 PRELIMINARY; PRT; 386 AA.
ID 09Y604;
AC 09Y604;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE TRAIL-R4-B.
GN TRAIL-R4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090091; PubMed=9430226;
RA Degli-Esposti M.A., Dougall W.C., Smolak P.J., Waugh J.Y., Smith C.A.,
RA Goodwin R.G.;
RT "The novel receptor TRAIL-R4 induces NF-kappaB and protects against
RT TRAIL-mediated apoptosis, yet retains an incomplete death domain.";
RL Immunity 7:813-820(1997).
DR EMBL; AF021233; AAC32766.1; -
DR HSSP; P19438; INCF.
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 386 AA; 41839 MW; BIC8D8A4B9DC7F5A CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 CRTGCPRGWVKV 167
DB 158 CRTGCPRGWVKV 169

RESULT 8
Q9UBN6 PRELIMINARY; PRT; 386 AA.
AC Q9UBN6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE DECOR RECEPTOR 2.
GN TRAIL-R4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98044290; PubMed=9382840;
RA Marsters S.A., Sheridan J.P., Pitti R.M., Huang A., Skubatch M.,
RA Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P.,
RA Ashkenazi A.;
RA Ashkenazi A.;
RT "A novel receptor for Apo2L/TRAIL contains a truncated death domain.";
RT Curr. Biol. 7:1003-1006(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX Marsters S.A., Sheridan J.P., Pitti R.M., Huang A., Skubatch M.,
RA Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P.,
RA Ashkenazi A.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090091; PubMed=9430226;
RA Degli-Esposti M.A., Dougall W.C., Smolak P.J., Waugh J.Y., Smith C.A.,
RA Goodwin R.G.;
RT "The novel receptor TRAIL-R4 induces NF-kappaB and protects against
RT TRAIL-mediated apoptosis, yet retains an incomplete death domain.";
RL Immunity 7:813-820(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98196860; PubMed=9537512;
RA Pan G., Ni J., Wei Y.F., Dixit V.M.;
RT "TRUND, a new member of the TRAIL receptor family that antagonizes
RT TRAIL signalling.";
RL FEBS Lett. 424:41-45(1998).
DR EMBL; AF029761; AAD03477.1; -
DR EMBL; AF021232; AAC32765.1; -
DR EMBL; AF023849; AAC52053.1; -

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DR HSSP; P19438; INCF.
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 386 AA; 41823 MW; 77A93577CAAF2632 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 CRTGCPRGWVKV 167
DB 158 CRTGCPRGWVKV 169

RESULT 9
O87342 PRELIMINARY; PRT; 920 AA.
ID O87342;
AC O87342;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE BETA-(1-3)-GLUCOSYL TRANSFERASE.
GN NDVB.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBL_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=USDA 110.
RA Bhagwat A.A., Keister D.L.;
RT "Site-Directed Mutagenesis of the beta-(1->3)-D-Glucan
RT Synthesis Locus of Bradyrhizobium japonicum.";
RL Mol. Plant Microbe Interact. 8:366-370(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=USDA 110.
RA Bhagwat A.A., Keister D.L.;
RT "Cyclic beta-1-3-glucan synthase.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047687; AAC62210.1; -
DR INTERPRO; IPR001173; -
DR PFAM; PF00355; Glycos_transf_2; 1.
KW transferase.
SQ SEQUENCE 920 AA; 102495 MW; A27FC1917DAF57CE CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 VVAAYLLVSA 51
DB 3 VVAAYLLVSA 13

RESULT 10
O67645 PRELIMINARY; PRT; 362 AA.
ID O67645;
AC O67645;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE GYCOPROTEIN 1.
OS gallid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBL_TaxID=10386;
RN [1]

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RP SEQUENCE FROM N.A.
 RC STRAIN=USDA CHALLENGE STRAIN;
 RX MEDLINE=97033380; PubMed=8679127;
 RA Wild M.A., Cook S., Cochran M.;
 RT "A genomic map of infectious laryngotracheitis virus and the sequence
 RT and organization of genes present in the unique short and flanking
 RT regions.";
 RL Virus Genes 12:107-116(1996).
 DR EMBL: U28832; AAC5101.1; -;
 DR INTERPRO: IPR002874; -;
 DR PFIAM: PF01688; Herpes_g1.1.
 SQ SEQUENCE 362 AA; 39750 MW; F530C1AA7CC6B5 CRC64;

Query Match 2.0%; Score 9; DB 14; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 IGVTAAYV 224
 DB 272 IGVTAAYV 280

RESULT 11
 ID 008065 PRELIMINARY; PRT; 29 AA.
 AC 008065;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE PUTATIVE PHOSPHOLIPID TRANSFER PROTEIN (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OC NCBI_TaxId=4577;
 RX MEDLINE=94105294; PubMed=8278499;
 RA Keith C.S., Hoang D.O., Barrett B.M., Feigelman B., Nelson M.C.,
 RA Thail H., Baysdorfer C.;
 RT "Partial sequence analysis of 130 randomly selected maize cDNA
 RT clones.";
 RL Plant Physiol. 101:329-332(1993).
 DR EMBL: M95074; AAA18561.1; -;
 FT NON_TER 29
 FT SEQUENCE 29 AA; 2767 MW; AF3D341B1B4259C6 CRC64;

Query Match 1.8%; Score 8; DB 10; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 VVAAYLL 48
 DB 12 VVAAYLL 19

RESULT 12
 ID 09LMO0 PRELIMINARY; PRT; 108 AA.
 AC 09LMO0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE EST AU065411(R3610) CORRESPONDS TO A REGION OF THE PREDICTED GENE.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
 OC NCBI_TaxId=4550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0451C06.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP001551; BAA92945.1; -;
 SQ SEQUENCE 108 AA; 10846 MW; 1768BA3625B367D0 CRC64;

Query Match 1.8%; Score 8; DB 10; Length 108;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VVAAYLLV 49
 DB 7 VVAAYLLV 14

RESULT 13
 ID 024583 PRELIMINARY; PRT; 121 AA.
 AC 024583;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OC NCBI_TaxId=4577;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B73;
 RA Betwar N.M., Hoang D., Baysdorfer C.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: PLANT NONSPECIFIC LIPID-TRANSFER PROTEINS TRANSFER
 CC PHOSPHOLIPIDS AS WELL AS GALACTOLIPIDS ACROSS MEMBRANES.
 CC -I- SIMILARITY: TO OTHER PLANTS LTP.
 DR EMBL: U66105; AAB06443.1; -;
 DR HSSP: P19656; IAGM.
 DR MENDEL: 27039; Zeama.1124;27039.
 DR INTERPRO: IPR000528; -;
 DR PFIAM: PF00279; LTP; 1.
 DR PRINTS: PR00382; LIPIDTRANSFER.
 DR PROSITE: PS00597; PLANT LTP; 1.
 KV Lipid-binding; Transport.
 FT DISULFID 103
 FT SEQUENCE 121 AA; 11726 MW; DC63478860C115B CRC64;

Query Match 1.8%; Score 8; DB 10; Length 121;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 VVAAYLL 48
 DB 12 VVAAYLL 19

RESULT 14
 ID 09KX88 PRELIMINARY; PRT; 223 AA.
 AC 09KX88;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE PUTATIVE SECRETED PROTEIN.
 GN SCC53.33C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxId=1902;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases;
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases;
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL MBL, Microbiol. 21:77-96(1996).
 DR EMBL, AL357591; CAB93462.1; -;
 SO SEQUENCE 223 AA; 24704 MW; 4DA48394012D5BDF CRC64;

Query Match 1.8%; Score 8; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 VLVVAAVL 46
 Db 16 VLVVAAVL 23

RESULT 15
 ID 09JUE5 PRELIMINARY; PRT; 257 AA.
 AC 09JUE5;
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)
 DE BRAIN CDNA, CLONE MNCB-0873, SIMILAR TO MUS MUSCULUS PSEUDOURIDINE
 DE SYNTHASE 1 (PUS1) MRNA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL;
 RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
 RA Hashimoto K.;
 RT "Isolation of full-length cDNA clones from mouse brain cDNA library
 RT made by oligo-capping method.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AB041563; BAA95047.1; -;
 SO SEQUENCE 257 AA; 28939 MW; 5C2AC7BC272D407C CRC64;

Query Match 1.8%; Score 8; DB 11; Length 257;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ARGPAPVP 35
 Db 19 ARGPAPVP 26

RESULT 16
 ID 014755 PRELIMINARY; PRT; 259 AA.
 AC 014755;
 DT 01-JAN-1998 (TREMUREL. 05, Created)
 DT 01-JAN-1998 (TREMUREL. 05, Last sequence update)
 DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)
 DE TRAIL RECEPTOR 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER, AND SPLEEN;
 RA Schneider P., Bodmer J.-L., Thome M., Holler N., Hofmann K.,
 RA Tschopp J.;
 RL FEBS Lett. 0:0-0(1997).
 DR EMBL, AF016267; AAB81181.1; -;
 DR HSSP: P19438; 1EXT.
 DR INTERPRO: IPR001368; -;
 DR PRAM: PF00020; TNFR_G6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 SO SEQUENCE 259 AA; 27365 MW; FE3BE82676EBD727 CRC64;

Query Match 1.8%; Score 8; DB 4; Length 259;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 SPENCRCRC 156
 Db 121 SPENCRCRC 128

RESULT 17
 ID 09RIW2 PRELIMINARY; PRT; 288 AA.
 AC 09RIW2;
 DT 01-MAY-2000 (TREMUREL. 13, Created)
 DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
 DT 01-JUN-2000 (TREMUREL. 14, Last annotation update)
 DE PUTATIVE TRANSMEMBRANE TRANSPORT PROTEIN (FRAGMENT).
 GN SC33.16.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID-1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Brown S.P., Harris D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL MBL, Microbiol. 21:77-96(1996).
 DR EMBL, AL121854; CAB58315.1; -;
 DR INTERPRO: IPR001734; -;
 DR TRANSMEMBRANE.
 FT NON_TER 288
 SO SEQUENCE 288 AA; 29488 MW; 826CF37AC6D3D5ED CRC64;

Query Match 1.8%; Score 8; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 VLVVAAVL 46
 Db 199 VLVVAAVL 206

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RESULT 18
ID 014798 PRELIMINARY: PRT: 299 AA.
AC 014798:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CYTOKINIC TRAIL RECEPTOR-3 (LYMPHOCYTE INHIBITOR OF TRAIL) (ANTAGONIST)
DE DECOY RECEPTOR FOR TRAIL/APO-2L.
CN TRAIL-R3 OR LIT OR TRID OR DCR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Macfarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
RA Cohen G.M., Alnemri E.S.;
RL J. Biol. Chem. 0:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-97461602; PubMed-9314565;
RA Degli-Esposti M.A., Smolak P.J., Walczak H., Waugh J., Huang C.P.,
RA Dubose R.F., Goodwin R.G., Smith C.A.;
RT "Cloning and characterization of TRAIL-R3, a novel member of the
RT emerging TRAIL receptor family.";
RL J. Exp. Med. 186:1165-1170(1997).
RN [3]
RP SEQUENCE OF 41-299 FROM N.A.
RA Mongkolsapaya J., Cowper A., Xu X., Morris G., McMichael A.J.,
RA Bell J.I., Screaton G.R.;
RL J. Immunol. 0:0-0(1997).
RN [4]
RP SEQUENCE OF 41-299 FROM N.A.
RA MEDLINE-97390508; PubMed-9242610;
RA Pan G., Ni J., Wei Y.F., Yu G., Gentz R., Dixit V.M.;
RT "An antagonist decoy receptor and a death domain-containing receptor
RT for TRAIL.";
RL Science 277:815-818(1997).
RN [5]
RP SEQUENCE OF 41-299 FROM N.A.
RA MEDLINE-97390509; PubMed-9242611;
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA Goddard A.D., Godowski P., Ashkenazi A.;
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT receptors.";
RL Science 277:818-821(1997).
DR EMBL: AF020502; AAB71413.1; -
DR EMBL: AF014794; AAC05593.1; -
DR EMBL: AF033854; AAB67506.1; -
DR EMBL: AF012628; AAB67110.1; -
DR EMBL: AF012536; AAB67104.1; -
DR HSSP: P19438; 1EXT.
DR INTERPRO: IPR001368; -
DR PFM: PF00020; TNR_C6; 2.
DR PROSITE: PS00652; TNR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS0050; TNR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 299 AA; 31759 MW; 2435106F847FE1AB CRC64;

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Query Match 1.8%; Score 8; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 149 SPEMCRKC 156
DB 161 SPEMCRKC 168

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RESULT 19
O97982

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ID 097982 PRELIMINARY: PRT: 341 AA.
AC 097982:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE MHC CLASS I ANTIGEN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA FUJIKI K., Nakao M., Nagai T., Shin D., Yano T.;
RA "cDNA cloning of a carp class I major histocompatibility antigen
RT variant.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB018581; BAA33884.1; -
DR INTERPRO: IPR001039; -
DR INTERPRO: IPR003006; -
DR PFM: PF00047; 187.1.
DR PFM: PF00129; MHC_I_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PRODOM: PD000050; -; 1.
KW MHC.
SQ SEQUENCE 341 AA; 38020 MW; 70F61AFCAD1FCDBE CRC64;

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Query Match 1.8%; Score 8; DB 7; Length 341;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 41 VVAAYVLL 48
DB 297 VVAAYVLL 304

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RESULT 20
ID 09LHX9 PRELIMINARY: PRT: 364 AA.
AC 09LHX9:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ESTS AU03277(S14085).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CV. NIPPONBAR;
RA Sasaki T., Matsunoto K.;
RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0515G01.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP001633; BAA94239.1; -
SQ SEQUENCE 364 AA; 38737 MW; 17DA203DD05ACC8C CRC64;

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Query Match 1.8%; Score 8; DB 10; Length 364;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 41 VVAAYVLL 48
DB 9 VVAAYVLL 16

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RESULT 21
O9L2C4 PRELIMINARY: PRT: 541 AA.
O9L2C4

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AC G9L2C4;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE PUTATIVE MEMBRANE PROTEIN (FRAGMENT).
 GN SC7A8.34.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Kienast M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Kienast H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; AL137187; CAB69783.1; -;
 FT NON_TER. 541 541
 SQ SEQUENCE 541 AA; 58208 MW; 0DF03D22010F199B CRC64;

Query Match 1.88; Score 8; DB: 2; Length 541;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 VVAAYLL 48
 |||||
 Db 94 VVAAYLL 101

RESULT 22
 ID 09W462 PRELIMINARY; PRT; 558 AA.
 AC 09W462;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE CG3016 PROTEIN.
 GN CG3016.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Butler H., Brokstein P., Brotlier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshneft A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Welnslock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003435; AAF6096.1; -;
 DR FLYBASE; FBgn0029819; CG3016.
 DR INTERPRO; IPR001394; -;
 DR PFM; PF00442; UCH-1; 1.
 DR PFM; PF00443; UCH-2; 1.
 SQ SEQUENCE 558 AA; 60879 MW; 86E46CC71D09EE75 CRC64;

Query Match 1.88; Score 8; DB: 5; Length 558;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 217 GVTAAAY 224
 |||||
 Db 11 GVTAAAY 18

RESULT 23
 ID 09SEP1 PRELIMINARY; PRT; 592 AA.
 AC 09SEP1;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE THREONINE DEHYDRATASE/DEAMINASE.
 GN OMR1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV; GMI1B;
 RA Mourad G.S., Emerick R.M., Smith A.M.;
 RT "Cloning and Sequencing of a cDNA Encoding an Isoleucine Feedback
 RT Insensitive Threonine Dehydratase/Deaminase of Arabidopsis thaliana
 RT line GMI1b (om1/cmr1)."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF177212; ADS4324.1; -;
 DR HSSP; P04968; ITDJ.
 DR INTERPRO; IPR000524; -;
 DR INTERPRO; IPR000634; -;
 DR INTERPRO; IPR001721; -;
 DR INTERPRO; IPR001925; -;
 DR PFM; PF00291; PALP; 1.
 DR PFM; PF00585; Thr_dehydrat_C; 2.
 DR PROSITE; PS00043; HTH_GNTR_FAMILY; UNKNOWN_1.

DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
SQ SEQUENCE 592 AA; 64562 MW; ID02F73AD53FAF6C CRC64;

Query Match 1.8%; Score 8; DB 10; Length 592;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 283 QVPEQEME 290
|||||
DB 558 QVPEQEME 565

RESULT 24
O9ZSS6 PRELIMINARY; PRT; 592 AA.
ID O9ZSS6;
AC O9ZSS6;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE THREONINE DEHYDRATASE/DEAMINASE (EC 4.2.1.16).
GN OMRI OR T22K18.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Kosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Mourad G., Emerick R., Marion A., Smith A.;
RT "Cloning and Sequencing of a cDNA Encoding Threonine
dehydratase/Deaminase of Arabidopsis thaliana (Accession No. AF096281)
(pGR 98-199)."
RL Plant Physiol. 118:1534-1534(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Romling C.M., Koo H., Fujii C.Y., Ulterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence";
RL Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Mourad G.S., Smith A.M.;
RT "Molecular characterization of the genomic clone, including the
promoter sequences, of threonine dehydratase/deaminase from
Arabidopsis thaliana";
RL Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096281; AAC97936.1; -;
DR EMBL; AC010927; AAF04418.1; -;
DR EMBL; AF221984; AAF33370.1; -;
DR HSSP; P04968; 1TDJ.
DR INTERPRO; IPR000524; -;
DR INTERPRO; IPR000634; -;
DR INTERPRO; IPR001721; -;
DR INTERPRO; IPR001926; -;
DR PFAM; PF00291; PALP; 1.
DR PFAM; PF00585; Thr_dehydrat.C; 2.
DR PROSITE; PS00043; HTH_GNTR_FAMILY; UNKNOWN_1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KM Lyase.
SQ SEQUENCE 592 AA; 64634 MW; 16658747052FAE7C CRC64;

Query Match 1.8%; Score 8; DB 10; Length 592;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 283 QVPEQEME 290
|||||
DB 558 QVPEQEME 565

RESULT 25

P87363 PRELIMINARY; PRT; 708 AA.
ID P87363;
AC P87363;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE FTBRILLIN-1 (FRAGMENT).
GN FBNI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Price C., Godfrey M.;
RL Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88872; AAB48531.1; -;
DR HSSP; P07204; 1FGD.
DR INTERPRO; IPR000152; -;
DR INTERPRO; IPR000561; -;
DR INTERPRO; IPR001491; -;
DR INTERPRO; IPR001881; -;
DR INTERPRO; IPR002212; -;
DR PFAM; PF00008; EGF; 14.
DR PFAM; PF00683; TB; 2.
DR PRINTS; PR00907; THROMBODULN.
DR PROSITE; PS00010; ASX_HYDROXYL; 13.
DR PROSITE; PS01186; EGF_2; 10.
DR PROSITE; PS01187; EGF_CA; 13.
KW Glycoprotein; EGF-like domain.
FT NON_TER
SQ SEQUENCE 708 AA; 76163 MW; C247271C1DF73361 CRC64;

Query Match 1.8%; Score 8; DB 13; Length 708;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 CPPGHHS 88
|||||
DB 163 CPPGHHS 170

RESULT 26

O9L092 PRELIMINARY; PRT; 743 AA.
ID O9L092;
AC O9L092;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.
GN SCC24.25.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Brown S.P., Harris D.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);

Query Match 1.8%; Score 8; DB 13; Length 708;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; AL163003; CAB86119.1; -;
 SQ SEQUENCE 743 AA; 77472 MW; 7FAF0A35D021489E CRC64;

Query Match 1.8%; Score 8; DB 2; Length 743;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LVLVVAAY 45
 |||||
 Db 15 LVLVVAAY 22

RESULT 27
 ID 024971 PRELIMINARY; PRT; 769 AA.
 AC 024971;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE VARIANT-SPECIFIC SURFACE PROTEIN.
 OS VSPA6-S2
 OS Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
 OX NCBI_TaxID=5741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WA6;
 RA Yang Y., Adam R.D.;
 RL Infect. Immun. 0:0-0(0).
 DR EMBL; U17981; AAA82586.1; -;
 DR INTERPRO; IPR000345; -;
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN.1.
 SQ SEQUENCE 769 AA; 78698 MW; C57C7065A15AEC2 CRC64;

Query Match 1.8%; Score 8; DB 5; Length 769;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 KTGSDASY 399
 |||||
 Db 589 KTGSDASY 596

RESULT 28
 ID 092530 PRELIMINARY; PRT; 3013 AA.
 AC 092530;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OX Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VN235;
 RA Okamoto H.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VN235;
 RX MEDLINE=98378034; PubMed=9714232;
 RA Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F., Miyakawa Y.,
 RA Mayumi M.;

RT "The entire nucleotide sequences of three hepatitis C virus isolates
 RT in genetic groups 7-9 and comparison with those in the other eight
 RT genetic groups";
 RL J. Gen. Virol. 79:1847-1857(1998).
 DR EMBL; D84263; BAA3265.1; -;
 DR HSSP; P27958; 1A1V.
 DR INTERPRO; IPR000745; -;
 DR INTERPRO; IPR001410; -;
 DR INTERPRO; IPR001490; -;
 DR INTERPRO; IPR002166; -;
 DR INTERPRO; IPR002518; -;
 DR INTERPRO; IPR002519; -;
 DR INTERPRO; IPR002521; -;
 DR INTERPRO; IPR002522; -;
 DR INTERPRO; IPR002531; -;
 DR INTERPRO; IPR002868; -;
 DR PFAM; PF00998; HCV_RdRp; 1.
 DR PFAM; PF01001; HCV_NS4b; 1.
 DR PFAM; PF01006; HCV_NS4a; 1.
 DR PFAM; PF01506; HCV_NS5a; 1.
 DR PFAM; PF01538; HCV_NS2; 1.
 DR PFAM; PF01539; HCV_env; 1.
 DR PFAM; PF01542; HCV_core; 1.
 DR PFAM; PF01543; HCV_capsid; 1.
 DR PFAM; PF01560; HCV_NS1; 1.
 DR PRODOM; PD186062; -; 1.
 KW Polyprotein.
 SQ SEQUENCE 3013 AA; 328197 MW; C9EE9C0231B86EAF CRC64;

Query Match 1.8%; Score 8; DB 14; Length 3013;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 SGEAPAVE 195
 |||||
 Db 1868 SGEAPAVE 1875

RESULT 29
 ID 079818 PRELIMINARY; PRT; 39 AA.
 AC 079818;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
 DE PX ORF-II (FRAGMENT).
 OS Human T-cell leukemia virus type II (HTLV-II).
 OC Viruses; Retrovirdae; Retroviridae; BLV-HTLV retroviruses.
 OX NCBI_TaxID=11909;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dube D.K., Sherman M.P., Saksena N.K., Bryz-Gorula V., Mendelson J.,
 RA Arnold C.B., Spicer T., Glaser J.B., Williams A.E., Nishimura M.,
 RA Jacobsen S., Polesz B.J.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M95092; AAA45437.1; -;
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4168 MW; 8CAA7668D8588695 CRC64;

Query Match 1.6%; Score 7; DB 14; Length 39;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 TSSPCTP 205
 |||||
 Db 33 TSSPCTP 39

RESULT 30
 085093

ID 085093 PRELIMINARY: PRT: 39 AA.
 AC 085093;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE TAX AND REX GENES (PARTIAL) (FRAGMENT).
 GN REX.
 OS Simian T-cell leukemia virus.
 OC Viruses; Retrovirdae; Retroviridae; BLV-RTLV retroviruses.
 NCBI_TaxID=39101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-STLV-PP 1664, PARTIAL TAX/REX GENE;
 RA MEDLINE=94301105; PubMed=7913178;
 RX Liu H.F., Vandamme A.M., Van Brüssel M., Desmyter J., Goubau P.,
 RT "New retroviruses in human and simian T-lymphotropic viruses.";
 RL Lancet 344:265-266(1994).
 DR EMBL: Z32851; CAA83685.1; -.
 FT NON_TER 1 1
 FT 39 39
 SQ SEQUENCE 39 AA; 3957 MW; CCE/F74AE78A8783 CRC64;

Query Match 1.6%; Score 7; DB 14; Length 39;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 TSSPGRP 205
 [1]
 DB 33 TSSPGRP 39

RESULT 31
 O9KGS9 PRELIMINARY: PRT: 47 AA.
 AC 09KGS9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE CYTOCHROME C MATURATION PROTEIN (FRAGMENT).
 GN CCMC.
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 AC Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kwon E., Page W.J.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF285160; AAF87253.1; -.
 FT NON_TER 47 47
 FT 47 47
 SQ SEQUENCE 47 AA; 5488 MW; 2828B51DCDA95F9 CRC64;

Query Match 1.6%; Score 7; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VAAVILL 48
 [1]
 DB 28 VAAVILL 34

RESULT 32
 O45259 PRELIMINARY: PRT: 73 AA.
 AC 045259;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
 DE ORF73.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Bradyrhizobium group; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-USDA3, 11B110SPC4;
 RA Edeling S.;
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X13691; CAA31981.1; -.
 SQ SEQUENCE 73 AA; 8019 MW; A7B7E7B6CADD246 CRC64;

Query Match 1.6%; Score 7; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 LVLVAA 44
 [1]
 DB 62 LVLVAA 68

RESULT 33
 O32424 PRELIMINARY: PRT: 75 AA.
 AC 032424;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE FIMBRIAL PROTEIN.
 GN FAP.
 OS Actinobacillus actinomycetemcomitans
 OS (Haemophilus actinomycetemcomitans).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 AC Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=310A;
 RX MEDLINE=97392725; PubMed=9245617;
 RA Ishihara K., Honma K., Miura T., Kato T., Okuda K.;
 RT "Cloning and sequence analysis of the fimbriae associated protein
 (fap) gene from Actinobacillus actinomycetemcomitans.";
 RL Microb. Pathog. 23:65-69(1997).
 DR EMBL: D83053; BAA21831.1; -.
 SQ SEQUENCE 75 AA; 7971 MW; 1FEC8B7C040BDAT7F CRC64;

Query Match 1.6%; Score 7; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLVAVF 230
 [1]
 DB 41 VLVAVF 47

RESULT 34
 O66149 PRELIMINARY: PRT: 75 AA.
 AC 066149;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE FIMBRIAL PROTEIN FLP PRECURSOR.
 GN FLP OR FAPATCC29523 OR FAP301A OR FAP310A OR FAP312A OR FAP3A3.
 OS Actinobacillus actinomycetemcomitans
 OS (Haemophilus actinomycetemcomitans).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 AC Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98285392; PubMed=9623911;
 RA Inoue T., Tanimoto I., Ohta H., Kato K., Murayama Y., Fukui K.;

RT "Molecular characterization of low-molecular-weight component protein,
RT FLP, in *Actinobacillus actinomycetemcomitans* fimbriae";
RL Microbiol. Immunol. 42:253-258(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RA Kokeguchi S., Hongyo H., Mirosue M., Sawada K., Takashiba S.,
RA Murayama Y.;
RT "Comparative analysis of fimbriae associated protein genes of
RT *Actinobacillus actinomycetemcomitans*.";
DR EMBL: AB012323; BAA7802.1; -;
DR EMBL: AB012318; BAA7802.1; -;
DR EMBL: AB012319; BAA7803.1; -;
DR EMBL: AB012320; BAA7804.1; -;
DR EMBL: AB012321; BAA7805.1; -;
DR EMBL: AB012322; BAA7806.1; -;
KW Signal.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 75 FIMBRIAL PROTEIN FLP.
SQ SEQUENCE 75 AA; 7998 MW; 1FEC8B69DE3BDA7F CRC64;

Query Match 1.6%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLIYAVF 230
Db 41 VLIYAVF 47

RESULT 35
O9WX51 PRELIMINARY; PRT; 75 AA.
ID O9WX51
AC O9WX51;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE FIMBRIAE ASSOCIATED PROTEIN PRECURSOR.
GN FAP0EN12-5A.
OS *Actinobacillus actinomycetemcomitans*
OS *(Haemophilus actinomycetemcomitans)*.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC *Actinobacillus*.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OEN12-5A;
RA Kokeguchi S., Hongyo H., Mirosue M., Sawada K., Takashiba S.,
RA Murayama Y.;
RT "Comparative analysis of fimbriae associated protein genes of
RT *Actinobacillus actinomycetemcomitans*.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB012325; BAA7809.1; -;
KW Signal.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 75 POTENTIAL.
SQ SEQUENCE 75 AA; 7938 MW; 1FEC8B74E2C8087F CRC64;

Query Match 1.6%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLIYAVF 230
Db 41 VLIYAVF 47

RESULT 36

O9S5J4
ID O9S5J4 PRELIMINARY; PRT; 75 AA.
AC O9S5J4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE FIMBRIAE ASSOCIATED PROTEIN PRECURSOR.
GN FAP5UNYAB67.
OS *Actinobacillus actinomycetemcomitans*
OS *(Haemophilus actinomycetemcomitans)*.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC *Actinobacillus*.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUNYAB 67;
RA Kokeguchi S., Hongyo H., Mirosue M., Sawada K., Takashiba S.,
RA Murayama Y.;
RT "Comparative analysis of fimbriae associated protein genes of
RT *Actinobacillus actinomycetemcomitans*.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB012324; BAA7808.1; -;
KW Signal.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 75 POTENTIAL.
SQ SEQUENCE 75 AA; 8025 MW; 1FF6A269DE3BDA7F CRC64;

Query Match 1.6%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLIYAVF 230
Db 41 VLIYAVF 47

RESULT 37
O9WM48
ID O9WM48 PRELIMINARY; PRT; 76 AA.
AC O9WM48;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE FIMBRIAE ASSOCIATED PROTEIN PRECURSOR.
GN FAPNCR9710 OR FAP212A OR FAPB4 OR FAP0H22-1A OR FAP0H45-10A.
OS *Actinobacillus actinomycetemcomitans*
OS *(Haemophilus actinomycetemcomitans)*.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC *Actinobacillus*.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NCTC9710, 212A, B4, B5, OHN22-1A, OHN45-10A;
RA Kokeguchi S., Hongyo H., Mirosue M., Sawada K., Takashiba S.,
RA Murayama Y.;
RT "Comparative analysis of fimbriae associated protein genes of
RT *Actinobacillus actinomycetemcomitans*.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB012316; BAA7800.1; -;
DR EMBL: AB012311; BAA7795.1; -;
DR EMBL: AB012312; BAA7796.1; -;
DR EMBL: AB012313; BAA7797.1; -;
DR EMBL: AB012314; BAA7798.1; -;
DR EMBL: AB012315; BAA7799.1; -;
KW Signal.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 76 POTENTIAL.
SQ SEQUENCE 76 AA; 8112 MW; 3D5FF6A269DE3BDA CRC64;

Query Match 1.6%; Score 7; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 42;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 224 LVIVAVF 230
 DB 41 LVIVAVF 47

RESULT 38
 Q9JOT2 PRELIMINARY; PRT; 89 AA.
 AC Q9JOT2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 GN RPSO OR NMA0815 OR NMB0609.
 OS Neisseria meningitidis (serogroup A), and
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699, 491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE-202256; PubMed-10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491."
 RL Nature 404:502-506(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MC58 / SEROGROUP B;
 RX MEDLINE-2017575; PubMed-10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwin M.L., Debey R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
 RA Cotton M.D., Ulfteback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scariato V., Masignani V., Pizsa M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58."
 RL Science 287:1809-1815(2000).
 DR EMBL: AL162754; CAB84097.1; -;
 DR EMBL: AE002416; AAF41036.1; -;
 DR TIGR: NMB0609; -;
 KN Ribosomal protein.
 SQ SEQUENCE 89 AA; 10386 MM; CF29ABE602503B01 CRC64;

Query Match 1.6%; Score 7; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 SQRRL 326
 DB 61 SQRRL 67

RESULT 39
 Q9LTR4 PRELIMINARY; PRT; 96 AA.
 AC Q9LTR4;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 GN GENOMIC DNA, CHROMOSOME 5, BAC CLONE:FL1/P19.
 OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
 RA Tabata S.;
 RT Structural analysis of Arabidopsis thaliana chromosome 5. XI.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB025603; BAA97459.1; -;
 SQ SEQUENCE 96 AA; 10069 MM; B4E7BFE4230E8BF CRC64;

Query Match 1.6%; Score 7; DB 10; Length 96;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LVIVAA 44
 DB 21 LVIVAA 27

RESULT 40
 Q65977 PRELIMINARY; PRT; 97 AA.
 AC Q65977;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
 GN ORF 4.
 OS Cassava common mosaic virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
 OX NCBI_TaxID=39046;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRAZILIAN;
 RX MEDLINE-9617336; PubMed-8601791;
 RA Calvert L.A., Cuervo M.T., Ospina M.D., Fauquet C.M., Ramirez B.C.;
 RT "Characterization of cassava common mosaic virus and a defective RNA
 species."
 RL J. Gen. Virol. 77:525-530(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRAZILIAN;
 RA Calvert L.A., Cuervo M.T., Ospina M.D., Fauquet C.M., Ramirez B.C.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U23414; AAC54778.1; -;
 SQ SEQUENCE 97 AA; 10083 MM; 077F8332CFA2FFC6 CRC64;

Query Match 1.6%; Score 7; DB 14; Length 97;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 LVVAAVL 46
 DB 39 LVVAAVL 45

RESULT 41
 Q26203 PRELIMINARY; PRT; 103 AA.
 AC Q26203;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 GN HYPOTHETICAL 12.0 KDA PROTEIN.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacterium.

OX NCB1_TaxID=2166;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE-98037514; PubMed-9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lum W., Pochler B., Qiu D.,
 RA Spadefora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-T., Rice P., Nolling J., Reeve J.N.;
 RT "Complete genome sequence of *Mechanobacterium thermocautophilicum*
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL: AE000800; AAB84599.1; -;
 KM Hypothetical protein
 SO SEQUENCE 103 AA; 12011 MW; 2B148B742A4AB867 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 LITQDOL 61
 [111111]
 DB 36 LITQDOL 42

RESULT 42
 O35152 PRELIMINARY; PRT; 111 AA.
 AC 035152;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE GS15.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xu Y., Wong S.H., Zhang T., Subramaniam V.N., Hong W.;
 RL J. Biol. Chem. 0:0-0(1997).
 DR EMBL: AF003988; AAB66320.1; -;
 DR INTERPRO: IPR000727; -;
 SO SEQUENCE 111 AA; 12417 MW; 905EDA73F6AEB4B4 CRC64;

Query Match 1.6%; Score 7; DB 11; Length 111;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 AVVLIVA 228
 [111111]
 DB 92 AVVLIVA 98

RESULT 43
 O35153 PRELIMINARY; PRT; 111 AA.
 AC 035153;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE GS15.
 OS *Mus musculus* (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Xu Y., Wong S.H., Zhang T., Subramaniam V.N., Hong W.;
 RL J. Biol. Chem. 0:0-0(1997).
 DR EMBL: AF003999; AAB66321.1; -;
 DR INTERPRO: IPR000727; -;
 SO SEQUENCE 111 AA; 12428 MW; 854B3523B71BE5BE CRC64;

Query Match 1.6%; Score 7; DB 11; Length 111;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 AVVLIVA 228
 [111111]
 DB 92 AVVLIVA 98

RESULT 44
 O9PE78 PRELIMINARY; PRT; 123 AA.
 ID O9PE78;
 AC O9PE78;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHEICAL PROTEIN XF1150.
 GN XF1150.
 OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OC NCB1_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-9A5C;
 RX MEDLINE-20365717; PubMed-10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Agencio M.,
 RA Alvaranga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
 RA Barrios M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
 RA Coutinho N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Fetto J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Gardner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohnel J.D., Jungueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA de Oliveira M.C., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Peixoto B.R., Pereira P.G., Rodrigues V., de Rosa A.J.M.,
 RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Teal S.M., Tsunako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Zedler J., Setubal J.C., Vettore A.L.,
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
 RL Nature 406:151-157(2000).
 DR EMBL: AE003950; AAF83960.1; -;
 KM Hypothetical protein.
 SO SEQUENCE 123 AA; 12962 MW; EC6835F9FCF5CE47 CRC64;

Query Match 1.6%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 LSGIITG 217
 [111111]
 DB 104 LSGIITG 110

RESULT 45
 ID 053859 PRELIMINARY; PRT; 130 AA.
 AC 053859;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE HYPOTHEICAL 13.5 KDA PROTEIN.
 GN RV0847 OR MT043.40.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham D., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellern S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544 (1998).
 DR EMBL; AL022004; CAAL1653.1;
 DR TUBERCULIST; RV0847;
 KW Hypothetical protein.
 SQ SEQUENCE 130 AA; 13519 MW; CB443C14F32A27BD CRC64;

Query Match 1.6%; Score 7; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 217 GVTVAAY 223
 Db 14 GVTVAAY 20
 RESULT 46
 ID 088389 PRELIMINARY; PRT; 131 AA.
 AC 088389;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE REX PROTEIN (FRAGMENT).
 OS Simian T-cell leukemia virus.
 OC Viruses; Retroid viruses; Retroviridae; BLV-HTLV retroviruses.
 OX NCBI_TaxID=39101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEQUENCED USING A PCR FRAGMENT;
 RX MEDLINE=96201457; PubMed=8609475;
 RA Vandamme A.M., Liu H.F., Van Brussel M., Meurichy W.D., Desmyter J.,
 RA Goubau P.;
 RT "The presence of a divergent T-lymphotropic virus in a wild-caught
 RT pygmy chimpanzee (Pan paniscus) supports an African origin for the
 RT human T-lymphotropic/simian T-lymphotropic group of viruses.";
 RL J. Gen. Virol. 77:1089-1099 (1996).
 RN [2]
 RP SEQUENCE OF 1-40 FROM N.A.
 RC STRAIN-SEQUENCED USING A PCR FRAGMENT;
 RX MEDLINE=94301105; PubMed=7913178;
 RA Liu H.F., Vandamme A.M., Van Brussel M., Desmyter J., Goubau P.;
 RT "New retroviruses in human and simian T-lymphotropic viruses.";
 RL Lancet 344:265-266 (1994).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEQUENCED USING A PCR FRAGMENT;
 RA Vandamme A.M.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 246344; CAAB6463.1;
 DR INTERPRO; IPR002965;
 DR PRINTS; PRO1217; PRICEXTENSN.
 FT NON_TER 1
 SQ SEQUENCE 131 AA; 13386 MW; 54D2465325918DDB CRC64;

Query Match 1.6%; Score 7; DB 14; Length 131;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 TSSPGTP 205
 Db 33 TSSPGTP 39

RESULT 47
 ID 09X215 PRELIMINARY; PRT; 132 AA.
 AC 09X215;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN TM1872.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser J.C.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima."
 RL Nature 393:323-329 (1999).
 DR EMBL; AE001824; AAD36934.1;
 DR TIGR; TM1872;
 DR INTERPRO; IPR001602;
 DR PFAM; PF01894; UPF0047; 1.
 DR PROSITE; PS01314; UPF0047; 1.
 SQ SEQUENCE 132 AA; 14364 MW; C7648167A6F1C6CC CRC64;

Query Match 1.6%; Score 7; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 431 LEGNADS 437
 Db 78 LEGNADS 84

RESULT 48
 ID 066299 PRELIMINARY; PRT; 143 AA.
 AC 066299;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ALPHA SUBUNIT OF DINITROGENASE REDUCTASE (FE PROTEIN) (FRAGMENT).
 GN NIFH.
 OS unidentified nitrogen-fixing bacteria.

OC Bacteria.
OX NCB1_TaxID=34107;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohkuma M., Noda S., Kudo T.;
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB011848; BAA28385.1; -
DR HSSP; P00456; ICP2.
DR INTERPRO; IPR000392; -
DR PFAM; PF00142; fcr4.N1fh; 1.
DR PROSITE; PS00692; N1FH_FRXC_2; 1.
DR PROSITE; PS00746; N1FH_FRXC_1; 1.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15328 MW; D278B8AB19F02DAB CRC64;

Query Match 1.6%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 TTTNTV 136
Db 2 TTTNTV 8

RESULT 49
059825 PRELIMINARY; PRT; 146 AA.
AC 059825;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1).
GN SOXH.
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Sulfobactales; Sulfobactaceae; Sulfolobus.
OX NCB1_TaxID=2285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DSM 639;
RX MEDLINE-95333177; PubMed-7608970;
RA Castresana J., Iuebben M., Saraste M.;
RT "New archaeobacterial genes coding for redox proteins: implications for the evolution of aerobic metabolism";
RL J. Mol. Biol. 250:202-210(1995).
CC -1- FUNCTION: SUBUNIT I AND II FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA HEME A AND CU(A) TO THE BINDING CENTER FORMED BY HEME A3 AND CU(B). SUBUNIT II BINDS CU(A) AND CYTOCHROME C.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 FERROCYTOCHROME C.
CC -1- CORRECTOR: COPPER A AND HEME GROUP.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. (MITOCHONDRIAL).
CC -1- SIMILARITY: TO OTHER MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
DR EMBL; Z48338; CAA88320.1; -
DR HSSP; P18400; ICYX.
DR INTERPRO; IPR001505; -
DR INTERPRO; IPR002429; -
DR PFAM; PF00116; COX2; 1.
DR PROSITE; PS00078; COX2; 1.
DR PRODOM; PD000131; -; 1.
KW Oxidoreductase; Copper; Transmembrane.
FT METAL 90 90 COPPER A (PROBABLE).
FT METAL 94 94 COPPER A (PROBABLE).
FT METAL 98 98 COPPER A (PROBABLE).
SQ SEQUENCE 146 AA; 16336 MW; 70827C6CDD41FFE CRC64;

Query Match 1.6%; Score 7; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 AAVLVY 227
Db 15 AAVLVY 21

RESULT 50
082405 PRELIMINARY; PRT; 149 AA.
ID 082405
AC 082405;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE T-CELL LYMPHOTROPIC VIRUS TYPE 2 REX AND TAX GENES, PARTIAL CDS, DE CLONE PAR PX (FRAGMENT).
GN REX.
OS Human T-cell leukemia virus type II (HTLV-II).
OC Viruses; Retroid viruses; Retroviridae; BLV-HTLV retroviruses.
OX NCB1_TaxID=11909;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96190544; PubMed-8627666;
RA Ishaku N., Novoa P., Monken C., Oliveira M.D., Oliveira O.D.,
RA Ishak R., Oliveira M.P., Laureiro P., Ishak M., Acevedo V.,
RA Hamershtak N., Zhu S.W., Kudo T., Hall W.W.;
RT "Identification and characterization of a new and distinct molecular subtype of human T-cell lymphotropic virus type 2.";
RL J. Virol. 70:1481-1492(1996).
DR EMBL; U32880; AAB04919.1; -
FT NON_TER 1 1
SQ SEQUENCE 149 AA; 15672 MW; EDD87412BEABD565 CRC64;

Query Match 1.6%; Score 7; DB 14; Length 149;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 TSSPGT 205
Db 51 TSSPGT 57

Search completed: May 23, 2001, 14:22:12
Job time: 111 sec

